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(54) Title: NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED HUMAN G PROTEIN-COUPLED RECEPTORS

(57) Abstract

The invention disclosed in this patent document relates to transmembrane receptors, more particularly to a human G protein-coupled receptor for which the endogenous ligand is unknown ("orphan GPCR receptors"), and most particularly to mutated (non-endogenous) versions of the human GPCRs for evidence of constitutive activity.

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**NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED
HUMAN G PROTEIN-COUPLED RECEPTORS**

This patent application is a continuation-in-part of, and claims priority from, U.S. Serial Number 09/170,496, filed with the United States Patent and Trademark Office on
5 October 13, 1998. This application also claims the benefit of priority from the following provisional applications, all filed via U.S. Express Mail with the United States Patent and Trademark Office on the indicated dates: U.S. Provisional Number 60/110,060, filed November 27, 1998; U.S. Provisional Number 60/120,416, filed February 16, 1999; U.S. Provisional Number 60/121,852, filed February 26, 1999 claiming benefit of U.S.
10 Provisional Number 60/109,213, filed November 20, 1998; U.S. Provisional Number 60/123,944, filed March 12, 1999; U.S. Provisional Number 60/123,945, filed March 12, 1999; U.S. Provisional Number 60/123,948, filed March 12, 1999; U.S. Provisional Number 60/123,951, filed March 12, 1999; U.S. Provisional Number 60/123,946, filed March 12, 1999; U.S. Provisional Number 60/123,949, filed March 12, 1999; U.S.
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20

FIELD OF THE INVENTION

The invention disclosed in this patent document relates to transmembrane receptors, and more particularly to human G protein-coupled receptors, and specifically to

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GPCRs that have been altered to establish or enhance constitutive activity of the receptor. Preferably, the altered GPCRs are used for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having potential applicability as therapeutic agents.

5 BACKGROUND OF THE INVENTION

Although a number of receptor classes exist in humans, by far the most abundant and therapeutically relevant is represented by the G protein-coupled receptor (GPCR or GPCRs) class. It is estimated that there are some 100,000 genes within the human genome, and of these, approximately 2%, or 2,000 genes, are estimated to code for GPCRs. Receptors, including GPCRs, for which the endogenous ligand has been identified are referred to as "known" receptors, while receptors for which the endogenous ligand has not been identified are referred to as "orphan" receptors. GPCRs represent an important area for the development of pharmaceutical products: from approximately 20 of the 100 known GPCRs, 60% of all prescription pharmaceuticals have been developed.

15 GPCRs share a common structural motif. All these receptors have seven sequences of between 22 to 24 hydrophobic amino acids that form seven alpha helices, each of which spans the membrane (each span is identified by number, *i.e.*, transmembrane-1 (TM-1), transmembrane-2 (TM-2), etc.). The transmembrane helices are joined by strands of amino acids between transmembrane-2 and transmembrane-3, transmembrane-4 and transmembrane-5, and transmembrane-6 and transmembrane-7 on the exterior, or "extracellular" side, of the cell membrane (these are referred to as "extracellular" regions 1, 2 and 3 (EC-1, EC-2 and EC-3), respectively). The transmembrane helices are also joined by strands of amino acids between transmembrane-1 and transmembrane-2, transmembrane-3 and transmembrane-4, and

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transmembrane-5 and transmembrane-6 on the interior, or "intracellular" side, of the cell membrane (these are referred to as "intracellular" regions 1, 2 and 3 (IC-1, IC-2 and IC-3), respectively). The "carboxy" ("C") terminus of the receptor lies in the intracellular space within the cell, and the "amino" ("N") terminus of the receptor lies in the extracellular space
5 outside of the cell.

Generally, when an endogenous ligand binds with the receptor (often referred to as "activation" of the receptor), there is a change in the conformation of the intracellular region that allows for coupling between the intracellular region and an intracellular "G-protein." It has been reported that GPCRs are "promiscuous" with respect to G proteins, *i.e.*,
10 that a GPCR can interact with more than one G protein. *See*, Kenakin, T., 43 *Life Sciences* 1095 (1988). Although other G proteins exist, currently, Gq, Gs, Gi, Gz and Go are G proteins that have been identified. Endogenous ligand-activated GPCR coupling with the G-protein begins a signaling cascade process (referred to as "signal transduction"). Under normal conditions, signal transduction ultimately results in cellular activation or cellular inhibition.
15 It is thought that the IC-3 loop as well as the carboxy terminus of the receptor interact with the G protein.

Under physiological conditions, GPCRs exist in the cell membrane in equilibrium between two different conformations: an "inactive" state and an "active" state. A receptor in an inactive state is unable to link to the intracellular signaling transduction
20 pathway to produce a biological response. Changing the receptor conformation to the active state allows linkage to the transduction pathway (via the G-protein) and produces a biological response.

A receptor may be stabilized in an active state by an endogenous ligand or a

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compound such as a drug. Recent discoveries, including but not exclusively limited to modifications to the amino acid sequence of the receptor, provide means other than endogenous ligands or drugs to promote and stabilize the receptor in the active state conformation. These means effectively stabilize the receptor in an active state by

5 simulating the effect of an endogenous ligand binding to the receptor. Stabilization by such ligand-independent means is termed "constitutive receptor activation."

SUMMARY OF THE INVENTION

Disclosed herein are non-endogenous versions of endogenous, human GPCRs and uses thereof.

10

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a representation of 8XCRE-Luc reporter plasmid (*see*, Example 4(c)3.)

Figures 2A and 2B are graphic representations of the results of ATP and ADP binding to endogenous TDAG8 (2A) and comparisons in serum and serum free media (2B).

15

Figure 3 is a graphic representation of the comparative signaling results of CMV versus the GPCR Fusion Protein H9(F236K):Gsa.

DETAILED DESCRIPTION

The scientific literature that has evolved around receptors has adopted a number of terms to refer to ligands having various effects on receptors. For clarity and consistency, the following definitions will be used throughout this patent document. To the

20 extent that these definitions conflict with other definitions for these terms, the following definitions shall control:

AGONISTS shall mean materials (*e.g.*, ligands, candidate compounds) that

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activate the intracellular response when they bind to the receptor, or enhance GTP binding to membranes.

AMINO ACID ABBREVIATIONS used herein are set out in Table A:

TABLE A		
5	ALANINE	ALA
	ARGININE	ARG
	ASPARAGINE	ASN
	ASPARTIC ACID	ASP
	CYSTEINE	CYS
10	GLUTAMIC ACID	GLU
	GLUTAMINE	GLN
	GLYCINE	GLY
	HISTIDINE	HIS
	ISOLEUCINE	ILE
15	LEUCINE	LEU
	LYSINE	LYS
	METHIONINE	MET
	PHENYLALANINE	PHE
	PROLINE	PRO
20	SERINE	SER
	THREONINE	THR
	TRYPTOPHAN	TRP
	TYROSINE	TYR
	VALINE	VAL

25 **PARTIAL AGONISTS** shall mean materials (*e.g.*, ligands, candidate compounds) that activate the intracellular response when they bind to the receptor to a lesser degree/extent than do agonists, or enhance GTP binding to membranes to a lesser degree/extent than do agonists.

ANTAGONIST shall mean materials (*e.g.*, ligands, candidate compounds) that
 30 competitively bind to the receptor at the same site as the agonists but which do not activate the intracellular response initiated by the active form of the receptor, and can thereby inhibit the intracellular responses by agonists or partial agonists. **ANTAGONISTS** do not diminish the baseline intracellular response in the absence of an agonist or partial agonist.

CANDIDATE COMPOUND shall mean a molecule (for example, and not limitation,

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a chemical compound) that is amenable to a screening technique. Preferably, the phrase "candidate compound" does not include compounds which were publicly known to be compounds selected from the group consisting of inverse agonist, agonist or antagonist to a receptor, as previously determined by an indirect identification process ("indirectly identified
5 compound"); more preferably, not including an indirectly identified compound which has previously been determined to have therapeutic efficacy in at least one mammal; and, most preferably, not including an indirectly identified compound which has previously been determined to have therapeutic utility in humans.

COMPOSITION means a material comprising at least one component; a
10 "pharmaceutical composition" is an example of a composition.

COMPOUND EFFICACY shall mean a measurement of the ability of a compound to inhibit or stimulate receptor functionality, as opposed to receptor binding affinity. Exemplary means of detecting compound efficacy are disclosed in the Example section of this patent document.

15 **CODON** shall mean a grouping of three nucleotides (or equivalents to nucleotides) which generally comprise a nucleoside (adenosine (A), guanosine (G), cytidine (C), uridine (U) and thymidine (T)) coupled to a phosphate group and which, when translated, encodes an amino acid.

CONSTITUTIVELY ACTIVATED RECEPTOR shall mean a receptor subject to
20 constitutive receptor activation. A constitutively activated receptor can be endogenous or non-endogenous.

CONSTITUTIVE RECEPTOR ACTIVATION shall mean stabilization of a receptor in the active state by means other than binding of the receptor with its endogenous

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ligand or a chemical equivalent thereof.

CONTACT or **CONTACTING** shall mean bringing at least two moieties together, whether in an in vitro system or an in vivo system.

DIRECTLY IDENTIFYING or **DIRECTLY IDENTIFIED**, in relationship to the
5 phrase "candidate compound", shall mean the screening of a candidate compound against a constitutively activated receptor, preferably a constitutively activated orphan receptor, and most preferably against a constitutively activated G protein-coupled cell surface orphan receptor, and assessing the compound efficacy of such compound. This phrase is, under no
circumstances, to be interpreted or understood to be encompassed by or to encompass the
10 phrase "indirectly identifying" or "indirectly identified."

ENDOGENOUS shall mean a material that a mammal naturally produces. **ENDOGENOUS** in reference to, for example and not limitation, the term "receptor," shall mean that which is naturally produced by a mammal (for example, and not limitation, a human) or a virus. By contrast, the term **NON-ENDOGENOUS** in this context shall mean
15 that which is not naturally produced by a mammal (for example, and not limitation, a human) or a virus. For example, and not limitation, a receptor which is not constitutively active in its endogenous form, but when manipulated becomes constitutively active, is most preferably referred to herein as a "non-endogenous, constitutively activated receptor." Both terms can be utilized to describe both "in vivo" and "in vitro" systems. For example, and not limitation,
20 in a screening approach, the endogenous or non-endogenous receptor may be in reference to an in vitro screening system. As a further example and not limitation, where the genome of a mammal has been manipulated to include a non-endogenous constitutively activated receptor, screening of a candidate compound by means of an in vivo system is viable.

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G PROTEIN COUPLED RECEPTOR FUSION PROTEIN and GPCR FUSION

PROTEIN, in the context of the invention disclosed herein, each mean a non-endogenous protein comprising an endogenous, constitutively activate GPCR or a non-endogenous, constitutively activated GPCR fused to at least one G protein, most preferably the alpha (α) subunit of such G protein (this being the subunit that binds GTP), with the G protein preferably being of the same type as the G protein that naturally couples with endogenous orphan GPCR. For example, and not limitation, in an endogenous state, if the G protein "G α " is the predominate G protein that couples with the GPCR, a GPCR Fusion Protein based upon the specific GPCR would be a non-endogenous protein comprising the GPCR fused to G α ; in some circumstances, as will be set forth below, a non-predominant G protein can be fused to the GPCR. The G protein can be fused directly to the c-terminus of the constitutively active GPCR or there may be spacers between the two.

HOST CELL shall mean a cell capable of having a Plasmid and/or Vector incorporated therein. In the case of a prokaryotic Host Cell, a Plasmid is typically replicated as a autonomous molecule as the Host Cell replicates (generally, the Plasmid is thereafter isolated for introduction into a eukaryotic Host Cell); in the case of a eukaryotic Host Cell, a Plasmid is integrated into the cellular DNA of the Host Cell such that when the eukaryotic Host Cell replicates, the Plasmid replicates. Preferably, for the purposes of the invention disclosed herein, the Host Cell is eukaryotic, more preferably, mammalian, and most preferably selected from the group consisting of 293, 293T and COS-7 cells.

INDIRECTLY IDENTIFYING or **INDIRECTLY IDENTIFIED** means the traditional approach to the drug discovery process involving identification of an endogenous ligand specific for an endogenous receptor, screening of candidate compounds against the

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receptor for determination of those which interfere and/or compete with the ligand-receptor interaction, and assessing the efficacy of the compound for affecting at least one second messenger pathway associated with the activated receptor.

INHIBIT or **INHIBITING**, in relationship to the term "response" shall mean that a
5 response is decreased or prevented in the presence of a compound as opposed to in the absence of the compound.

INVERSE AGONISTS shall mean materials (*e.g.*, ligand, candidate compound) which bind to either the endogenous form of the receptor or to the constitutively activated form of the receptor, and which inhibit the baseline intracellular response initiated by the
10 active form of the receptor below the normal base level of activity which is observed in the absence of agonists or partial agonists, or decrease GTP binding to membranes. Preferably, the baseline intracellular response is inhibited in the presence of the inverse agonist by at least 30%, more preferably by at least 50%, and most preferably by at least 75%, as compared with the baseline response in the absence of the inverse agonist.

15 **KNOWN RECEPTOR** shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has been identified.

LIGAND shall mean an endogenous, naturally occurring molecule specific for an endogenous, naturally occurring receptor.

MUTANT or **MUTATION** in reference to an endogenous receptor's nucleic acid
20 and/or amino acid sequence shall mean a specified change or changes to such endogenous sequences such that a mutated form of an endogenous, non-constitutively activated receptor evidences constitutive activation of the receptor. In terms of equivalents to specific sequences, a subsequent mutated form of a human receptor is considered to be equivalent to

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a first mutation of the human receptor if (a) the level of constitutive activation of the subsequent mutated form of a human receptor is substantially the same as that evidenced by the first mutation of the receptor; and (b) the percent sequence (amino acid and/or nucleic acid) homology between the subsequent mutated form of the receptor and the first mutation
5 of the receptor is at least about 80%, more preferably at least about 90% and most preferably at least 95%. Ideally, and owing to the fact that the most preferred cassettes disclosed herein for achieving constitutive activation includes a single amino acid and/or codon change between the endogenous and the non-endogenous forms of the GPCR, the percent sequence homology should be at least 98%.

10 **NON-ORPHAN RECEPTOR** shall mean an endogenous naturally occurring molecule specific for an endogenous naturally occurring ligand wherein the binding of a ligand to a receptor activates an intracellular signaling pathway.

ORPHAN RECEPTOR shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has not been identified or is not known.

15 **PHARMACEUTICAL COMPOSITION** shall mean a composition comprising at least one active ingredient, whereby the composition is amenable to investigation for a specified, efficacious outcome in a mammal (for example, and not limitation, a human). Those of ordinary skill in the art will understand and appreciate the techniques appropriate for determining whether an active ingredient has a desired efficacious outcome based upon the
20 needs of the artisan.

PLASMID shall mean the combination of a Vector and cDNA. Generally, a Plasmid is introduced into a Host Cell for the purposes of replication and/or expression of the cDNA as a protein.

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STIMULATE or **STIMULATING**, in relationship to the term "response" shall mean that a response is increased in the presence of a compound as opposed to in the absence of the compound.

VECTOR in reference to cDNA shall mean a circular DNA capable of incorporating
5 at least one cDNA and capable of incorporation into a Host Cell.

The order of the following sections is set forth for presentational efficiency and is not intended, nor should be construed, as a limitation on the disclosure or the claims to follow.

A. Introduction

The traditional study of receptors has always proceeded from the a priori assumption
10 (historically based) that the endogenous ligand must first be identified before discovery could proceed to find antagonists and other molecules that could affect the receptor. Even in cases where an antagonist might have been known first, the search immediately extended to looking for the endogenous ligand. This mode of thinking has persisted in receptor research even after the discovery of constitutively activated receptors. What has not been heretofore recognized
15 is that it is the active state of the receptor that is most useful for discovering agonists, partial agonists, and inverse agonists of the receptor. For those diseases which result from an overly active receptor or an under-active receptor, what is desired in a therapeutic drug is a compound which acts to diminish the active state of a receptor or enhance the activity of the receptor, respectively, not necessarily a drug which is an antagonist to the endogenous ligand.
20 This is because a compound that reduces or enhances the activity of the active receptor state need not bind at the same site as the endogenous ligand. Thus, as taught by a method of this invention, any search for therapeutic compounds should start by screening compounds against the ligand-independent active state.

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B. Identification of Human GPCRs

The efforts of the Human Genome project has led to the identification of a plethora of information regarding nucleic acid sequences located within the human genome; it has been the case in this endeavor that genetic sequence information has been made available without an understanding or recognition as to whether or not any particular genomic sequence does or may contain open-reading frame information that translate human proteins. Several methods of identifying nucleic acid sequences within the human genome are within the purview of those having ordinary skill in the art. For example, and not limitation, a variety of human GPCRs, disclosed herein, were discovered by reviewing the GenBank™ database, while other GPCRs were discovered by utilizing a nucleic acid sequence of a GPCR, previously sequenced, to conduct a BLAST™ search of the EST database. Table B, below, lists several endogenous GPCRs that we have discovered, along with a GPCR's respective homologous receptor.

TABLE B

	Disclosed Human Orphan GPCRs	Accession Number Identified	Open Reading Frame (Base Pairs)	Per Cent Homology To Designated GPCR	Reference To Homologous GPCR (Accession No.)
15	hARE-3	AL033379	1,260 bp	52.3% LPA-R	U92642
20	hARE-4	AC006087	1,119 bp	36% P2Y5	AF000546
	hARE-5	AC006255	1,104 bp	32% <i>Oryzias latipes</i>	D43633
	hGPR27	AA775870	1,128 bp		
	hARE-1	AI090920	999 bp	43% KIAA0001	D13626
25	hARE-2	AA359504	1,122 bp	53% GPR27	
	hPPR1	H67224	1,053 bp	39% EBI1	L31581
	hG2A	AA754702	1,113 bp	31% GPR4	L36148

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	hRUP3	AL035423	1,005 bp	30%	2133653
				<i>Drosophila</i>	
				<i>melanogaster</i>	
	hRUP4	AI307658	1,296 bp	32% pNPGPR	NP_004876
				28% and 29 %	AAC41276
				<i>Zebra fish</i> Ya	and
				and Yb,	AAB94616
				respectively	
	hRUP5	AC005849	1,413 bp	25% DEZ	Q99788
				23% FMLPR	P21462
	hRUP6	AC005871	1,245 bp	48% GPR66	NP_006047
5	hRUP7	AC007922	1,173 bp	43% H3R	AF140538
	hCHN3	EST 36581	1,113 bp	53% GPR27	
	hCHN4	AA804531	1,077 bp	32% thrombin	4503637
	hCHN6	EST 2134670	1,503 bp	36% edg-1	NP_001391
	hCHN8	EST 764455	1,029 bp	47%	D13626
				KIAA0001	
10	hCHN9	EST 1541536	1,077 bp	41% LTB4R	NM_000752
	hCHN10	EST 1365839	1,055 bp	35% P2Y	NM_002563

Receptor homology is useful in terms of gaining an appreciation of a role of the receptors within the human body. As the patent document progresses, we will disclose techniques for mutating these receptors to establish non-endogenous, constitutively activated versions of these receptors.

The techniques disclosed herein have also been applied to other human, orphan GPCRs known to the art, as will be apparent as the patent document progresses.

C. Receptor Screening

Screening candidate compounds against a non-endogenous, constitutively activated version of the human GPCRs disclosed herein allows for the direct identification of candidate compounds which act at this cell surface receptor, without requiring use of the receptor's endogenous ligand. By determining areas within the body where the endogenous version of human GPCRs disclosed herein is expressed and/or over-expressed, it is possible to determine related disease/disorder states which are associated with the expression and/or over-expression

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of the receptor; such an approach is disclosed in this patent document.

With respect to creation of a mutation that may evidence constitutive activation of the human GPCR disclosed herein is based upon the distance from the proline residue at which is presumed to be located within TM6 of the GPCR; this algorithmic technique is disclosed
5 in co-pending and commonly assigned patent document U.S. Serial Number 09/170,496, incorporated herein by reference. The algorithmic technique is not predicated upon traditional sequence "alignment" but rather a specified distance from the aforementioned TM6 proline residue. By mutating the amino acid residue located 16 amino acid residues from this residue (presumably located in the IC3 region of the receptor) to, most preferably, a lysine residue,
10 such activation may be obtained. Other amino acid residues may be useful in the mutation at this position to achieve this objective.

D. Disease/Disorder Identification and/or Selection

As will be set forth in greater detail below, most preferably inverse agonists to the non-endogenous, constitutively activated GPCR can be identified by the methodologies of this
15 invention. Such inverse agonists are ideal candidates as lead compounds in drug discovery programs for treating diseases related to this receptor. Because of the ability to directly identify inverse agonists to the GPCR, thereby allowing for the development of pharmaceutical compositions, a search for diseases and disorders associated with the GPCR is relevant. For example, scanning both diseased and normal tissue samples for the presence
20 of the GPCR now becomes more than an academic exercise or one which might be pursued along the path of identifying an endogenous ligand to the specific GPCR. Tissue scans can be conducted across a broad range of healthy and diseased tissues. Such tissue scans provide a preferred first step in associating a specific receptor with a disease and/or disorder. *See, for*

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example, co-pending application (docket number ARE-0050) for exemplary dot-blot and RT-PCR results of several of the GPCRs disclosed herein.

Preferably, the DNA sequence of the human GPCR is used to make a probe for (a) dot-blot analysis against tissue-mRNA, and/or (b) RT-PCR identification of the expression
5 of the receptor in tissue samples. The presence of a receptor in a tissue source, or a diseased tissue, or the presence of the receptor at elevated concentrations in diseased tissue compared to a normal tissue, can be preferably utilized to identify a correlation with a treatment regimen, including but not limited to, a disease associated with that disease. Receptors can equally well be localized to regions of organs by this technique. Based on
10 the known functions of the specific tissues to which the receptor is localized, the putative functional role of the receptor can be deduced.

E. Screening of Candidate Compounds

1. Generic GPCR screening assay techniques

When a G protein receptor becomes constitutively active, it binds to a G protein (*e.g.*,
15 Gq, Gs, Gi, Gz, Go) and stimulates the binding of GTP to the G protein. The G protein then acts as a GTPase and slowly hydrolyzes the GTP to GDP, whereby the receptor, under normal conditions, becomes deactivated. However, constitutively activated receptors continue to exchange GDP to GTP. A non-hydrolyzable analog of GTP, [³⁵S]GTPγS, can be used to monitor enhanced binding to membranes which express constitutively activated receptors.
20 It is reported that [³⁵S]GTPγS can be used to monitor G protein coupling to membranes in the absence and presence of ligand. An example of this monitoring, among other examples well-known and available to those in the art, was reported by Traynor and Nahorski in 1995. The preferred use of this assay system is for initial screening of candidate compounds because the

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system is generically applicable to all G protein-coupled receptors regardless of the particular G protein that interacts with the intracellular domain of the receptor.

2. Specific GPCR screening assay techniques

Once candidate compounds are identified using the "generic" G protein-coupled receptor assay (*i.e.*, an assay to select compounds that are agonists, partial agonists, or inverse agonists), further screening to confirm that the compounds have interacted at the receptor site is preferred. For example, a compound identified by the "generic" assay may not bind to the receptor, but may instead merely "uncouple" the G protein from the intracellular domain.

a. Gs, Gz and Gi.

10 Gs stimulates the enzyme adenylyl cyclase. Gi (and Gz and Go), on the other hand, inhibit this enzyme. Adenylyl cyclase catalyzes the conversion of ATP to cAMP; thus, constitutively activated GPCRs that couple the Gs protein are associated with increased cellular levels of cAMP. On the other hand, constitutively activated GPCRs that couple Gi (or Gz, Go) protein are associated with decreased cellular levels of cAMP. *See, generally,*
15 "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols, J.G. et al eds. Sinauer Associates, Inc. (1992). Thus, assays that detect cAMP can be utilized to determine if a candidate compound is, *e.g.*, an inverse agonist to the receptor (*i.e.*, such a compound would decrease the levels of cAMP). A variety of approaches known in the art for measuring cAMP can be utilized; a most preferred approach relies upon the use
20 of anti-cAMP antibodies in an ELISA-based format. Another type of assay that can be utilized is a whole cell second messenger reporter system assay. Promoters on genes drive the expression of the proteins that a particular gene encodes. Cyclic AMP drives gene expression by promoting the binding of a cAMP-responsive DNA binding protein or

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transcription factor (CREB) that then binds to the promoter at specific sites called cAMP response elements and drives the expression of the gene. Reporter systems can be constructed which have a promoter containing multiple cAMP response elements before the reporter gene, *e.g.*, β -galactosidase or luciferase. Thus, a constitutively activated Gs-linked receptor causes
5 the accumulation of cAMP that then activates the gene and expression of the reporter protein. The reporter protein such as β -galactosidase or luciferase can then be detected using standard biochemical assays (Chen et al. 1995).

b. Go and Gq.

10 Gq and Go are associated with activation of the enzyme phospholipase C, which in turn hydrolyzes the phospholipid PIP₂, releasing two intracellular messengers: diacylglycerol (DAG) and inistol 1,4,5-triphoisphate (IP₃). Increased accumulation of IP₃ is associated with activation of Gq- and Go-associated receptors. *See, generally*, "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols,
15 J.G. et al eds. Sinauer Associates, Inc. (1992). Assays that detect IP₃ accumulation can be utilized to determine if a candidate compound is, *e.g.*, an inverse agonist to a Gq- or Go-associated receptor (*i.e.*, such a compound would decrease the levels of IP₃). Gq-associated receptors can also been examined using an AP1 reporter assay in that Gq-dependent phospholipase C causes activation of genes containing AP1 elements; thus, activated Gq-
20 associated receptors will evidence an increase in the expression of such genes, whereby inverse agonists thereto will evidence a decrease in such expression, and agonists will evidence an increase in such expression. Commercially available assays for such detection are available.

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3. GPCR Fusion Protein

The use of an endogenous, constitutively activate orphan GPCR or a non-endogenous, constitutively activated orphan GPCR, for use in screening of candidate compounds for the direct identification of inverse agonists, agonists and partial agonists provide an interesting screening challenge in that, by definition, the receptor is active even in the absence of an endogenous ligand bound thereto. Thus, in order to differentiate between, *e.g.*, the non-endogenous receptor in the presence of a candidate compound and the non-endogenous receptor in the absence of that compound, with an aim of such a differentiation to allow for an understanding as to whether such compound may be an inverse agonist, agonist, partial agonist or have no affect on such a receptor, it is preferred that an approach be utilized that can enhance such differentiation. A preferred approach is the use of a GPCR Fusion Protein.

Generally, once it is determined that a non-endogenous orphan GPCR has been constitutively activated using the assay techniques set forth above (as well as others), it is possible to determine the predominant G protein that couples with the endogenous GPCR. Coupling of the G protein to the GPCR provides a signaling pathway that can be assessed. Because it is most preferred that screening take place by use of a mammalian expression system, such a system will be expected to have endogenous G protein therein. Thus, by definition, in such a system, the non-endogenous, constitutively activated orphan GPCR will continuously signal. In this regard, it is preferred that this signal be enhanced such that in the presence of, *e.g.*, an inverse agonist to the receptor, it is more likely that it will be able to more readily differentiate, particularly in the context of screening, between the receptor when it is contacted with the inverse agonist.

The GPCR Fusion Protein is intended to enhance the efficacy of G protein coupling

with the non-endogenous GPCR. The GPCR Fusion Protein is preferred for screening with a non-endogenous, constitutively activated GPCR because such an approach increases the signal that is most preferably utilized in such screening techniques. This is important in facilitating a significant "signal to noise" ratio; such a significant ratio is import preferred for
5 the screening of candidate compounds as disclosed herein.

The construction of a construct useful for expression of a GPCR Fusion Protein is within the purview of those having ordinary skill in the art. Commercially available expression vectors and systems offer a variety of approaches that can fit the particular needs of an investigator. The criteria of importance for such a GPCR Fusion Protein construct is
10 that the endogenous GPCR sequence and the G protein sequence both be in-frame (preferably, the sequence for the endogenous GPCR is upstream of the G protein sequence) and that the "stop" codon of the GPCR must be deleted or replaced such that upon expression of the GPCR, the G protein can also be expressed. The GPCR can be linked directly to the G protein, or there can be spacer residues between the two (preferably, no more than about 12,
15 although this number can be readily ascertained by one of ordinary skill in the art). We have a preference (based upon convenience) of use of a spacer in that some restriction sites that are not used will, effectively, upon expression, become a spacer. Most preferably, the G protein that couples to the non-endogenous GPCR will have been identified prior to the creation of the GPCR Fusion Protein construct. Because there are only a few G proteins that have been
20 identified, it is preferred that a construct comprising the sequence of the G protein (*i.e.*, a universal G protein construct) be available for insertion of an endogenous GPCR sequence therein; this provides for efficiency in the context of large-scale screening of a variety of different endogenous GPCRs having different sequences.

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As noted above, constitutively activated GPCRs that couple to Gi, Gz and Go are expected to inhibit the formation of cAMP making assays based upon these types of GPCRs challenging (*i.e.*, the cAMP signal decreases upon activation thus making the direct identification of, *e.g.*, inverse agonists (which would further decrease this signal), interesting).

- 5 As will be disclosed herein, we have ascertained that for these types of receptors, it is possible to create a GPCR Fusion Protein that is not based upon the endogenous GPCR's endogenous G protein, in an effort to establish a viable cyclase-based assay. Thus, for example, a Gz coupled receptor such as H9, a GPCR Fusion Protein can be established that utilizes a Gs fusion protein – we believe that such a fusion construct, upon expression, "drives" or "forces"
- 10 the non-endogenous GPCR to couple with, *e.g.*, Gs rather than the "natural" Gz protein, such that a cyclase-based assay can be established. Thus, for Gi, Gz and Go coupled receptors, we prefer that that when a GPCR Fusion Protein is used and the assay is based upon detection of adenylyl cyclase activity, that the fusion construct be established with Gs (or an equivalent G protein that stimulates the formation of the enzyme adenylyl cyclase).

15 **F. Medicinal Chemistry**

- Generally, but not always, direct identification of candidate compounds is preferably conducted in conjunction with compounds generated via combinatorial chemistry techniques, whereby thousands of compounds are randomly prepared for such analysis. Generally, the results of such screening will be compounds having unique core structures; thereafter, these
- 20 compounds are preferably subjected to additional chemical modification around a preferred core structure(s) to further enhance the medicinal properties thereof. Such techniques are known to those in the art and will not be addressed in detail in this patent document.

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G. Pharmaceutical compositions

Candidate compounds selected for further development can be formulated into pharmaceutical compositions using techniques well known to those in the art. Suitable pharmaceutically-acceptable carriers are available to those in the art; for example, see
5 Remington's Pharmaceutical Sciences, 16th Edition, 1980, Mack Publishing Co., (Oslo et al., eds.)

H. Other Utility

Although a preferred use of the non-endogenous versions the human GPCRs disclosed herein may be for the direct identification of candidate compounds as inverse agonists,
10 agonists or partial agonists (preferably for use as pharmaceutical agents), these versions of human GPCRs can also be utilized in research settings. For example, *in vitro* and *in vivo* systems incorporating GPCRs can be utilized to further elucidate and understand the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signaling
15 cascade. The value in non-endogenous human GPCRs is that their utility as a research tool is enhanced in that, because of their unique features, non-endogenous human GPCRs can be used to understand the role of these receptors in the human body before the endogenous ligand therefor is identified. Other uses of the disclosed receptors will become apparent to those in the art based upon, *inter alia*, a review of this patent document.

20

EXAMPLES

The following examples are presented for purposes of elucidation, and not limitation, of the present invention. While specific nucleic acid and amino acid sequences are disclosed herein, those of ordinary skill in the art are credited with the ability to make minor

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modifications to these sequences while achieving the same or substantially similar results reported below. The traditional approach to application or understanding of sequence cassettes from one sequence to another (*e.g.* from rat receptor to human receptor or from human receptor A to human receptor B) is generally predicated upon sequence alignment techniques whereby the sequences are aligned in an effort to determine areas of commonality. The mutational approach disclosed herein does not rely upon this approach but is instead based upon an algorithmic approach and a positional distance from a conserved proline residue located within the TM6 region of human GPCRs. Once this approach is secured, those in the art are credited with the ability to make minor modifications thereto to achieve substantially the same results (*i.e.*, constitutive activation) disclosed herein. Such modified approaches are considered within the purview of this disclosure

Example 1**ENDOGENOUS HUMAN GPCRS****1. Identification of Human GPCRs**

Certain of the disclosed endogenous human GPCRs were identified based upon a review of the GenBank™ database information. While searching the database, the following cDNA clones were identified as evidenced below (Table C).

TABLE C

	Disclosed Human Orphan GPCRs	Accession Number	Complete DNA Sequence (Base Pairs)	Open Reading Frame (Base Pairs)	Nucleic Acid SEQ.ID. NO.	Amino Acid SEQ.ID. NO.
20	hARE-3	AL033379	111,389 bp	1,260 bp	1	2
	hARE-4	AC006087	226,925 bp	1,119 bp	3	4
25	hARE-5	AC006255	127,605 bp	1,104 bp	5	6
	hRUP3	AL035423	140,094 bp	1,005 bp	7	8

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hRUP5	AC005849	169,144 bp	1,413 bp	9	10
hRUP6	AC005871	218,807 bp	1,245 bp	11	12
hRUP7	AC007922	158,858 bp	1,173 bp	13	14

Other disclosed endogenous human GPCRs were identified by conducting a BLAST™
 5 search of EST database (dbest) using the following EST clones as query sequences. The
 following EST clones identified were then used as a probe to screen a human genomic library
 (Table D).

TABLE D

10	Disclosed Human Orphan GPCRs	Query (Sequence)	EST Clone/ Accession No. Identified	Open Reading Frame (Base Pairs)	Nucleic Acid SEQ.ID.NO.	Amino Acid SEQ.ID.NO.
	hGPCR27	Mouse GPCR27	AA775870	1,125 bp	17	18
	hARE-1	TDAG	1689643 A1090920	999 bp	19	20
15	hARE-2	GPCR27	68530 AA359504	1,122 bp	21	22
	hPPR1	Bovine PPR1	238667 H67224	1,053 bp	23	24
	hG2A	Mouse 1179426	<i>See Example 2(a), below</i>	1,113 bp	25	26
	hCHN3	N.A.	EST 36581 (full length)	1,113 bp	27	28
	hCHN4	TDAG	1184934 AA804531	1,077 bp	29	30
20	hCHN6	N.A.	EST 2134670 (full length)	1,503 bp	31	32
	hCHN8	KIAA0001	EST 764455	1,029 bp	33	34
	hCHN 9	1365839	EST 1541536	1,077 bp	35	36
	hCHN10	Mouse EST 1365839	Human 1365839	1,005 bp	37	38
	hRUP4	N.A.	A1307658	1,296 bp	39	40
25		N.A. = "not applicable".				

2. Full Length Cloning

a. Human G2A

Mouse EST clone 1179426 was used to obtain a human genomic clone containing all

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but three amino acid G2A coding sequences. The 5' of this coding sequence was obtained by using 5'RACE, and the template for PCR was Clontech's Human Spleen Marathon-Ready™ cDNA. The disclosed human G2A was amplified by PCR using the G2A cDNA specific primers for the first and second round PCR as shown in SEQ.ID.NO.: 41 and SEQ.ID.NO.:42
5 as follows:

5'-CTGTGTACAGCAGTTCGCAGAGTG-3' (SEQ.ID.NO.: 41; 1st round PCR)

5'-GAGTGCCAGGCAGAGCAGGTAGAC-3' (SEQ.ID.NO.: 42; second round PCR).

PCR was performed using Advantage GC Polymerase Kit (Clontech; manufacturing instructions will be followed), at 94°C for 30 sec followed by 5 cycles of 94°C for 5 sec and
10 72°C for 4 min; and 30 cycles of 94° for 5 sec and 70° for 4 min. An approximate 1.3 Kb PCR fragment was purified from agarose gel, digested with Hind III and Xba I and cloned into the expression vector pRC/CMV2 (Invitrogen). The cloned-insert was sequenced using the T7 Sequenase™ kit (USB Amersham; manufacturer instructions followed) and the sequence was compared with the presented sequence. Expression of the human G2A was detected by
15 probing an RNA dot blot (Clontech; manufacturer instructions followed) with the P³²-labeled fragment.

b. CHN9

Sequencing of the EST clone 1541536 showed CHN9 to be a partial cDNA clone having only an initiation codon; *i.e.*, the termination codon was missing. When CHN9
20 was used to blast against data base (nr), the 3' sequence of CHN9 was 100% homologous to the 5' untranslated region of the leukotriene B4 receptor cDNA, which contained a termination codon in the frame with CHN9 coding sequence. To determine whether the 5' untranslated region of LTB4R cDNA was the 3' sequence of CHN9, PCR was performed using primers based upon the 5' sequence flanking the initiation codon found in CHN9 and

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the 3' sequence around the termination codon found in the LTB4R 5' untranslated region.

The 5' primer sequence utilized was as follows:

5'-CCCGAATTCCTGCTTGCTCCCAGCTTGGCCC-3' (SEQ.ID.NO.: 43; sense) and

5'-TGTGGATCCTGCTGTCAAAGGTCCCATTCGG-3' (SEQ.ID.NO.: 44; antisense).

- 5 PCR was performed using thymus cDNA as a template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 uM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 65°C for 1min and 72 °C for 1 min and 10 sec. A 1.1kb fragment consistent with the predicted size was obtained from PCR. This PCR fragment was subcloned into pCMV (*see below*) and
- 10 sequenced (*see*, SEQ.ID.NO.: 35).

c. RUP 4

The full length RUP4 was cloned by RT-PCR with human brain cDNA (Clontech) as templates:

5'-TCACAATGCTAGGTGTGGTC-3' (SEQ.ID.NO.: 45; sense) and

- 15 5'-TGCATAGACAATGGGATTACAG-3' (SEQ.ID.NO.: 46; antisense).

PCR was performed using TaqPlus Precision™ polymerase (Stratagene; manufacturing instructions followed) by the following cycles: 94°C for 2 min; 94°C 30 sec; 55°C for 30 sec, 72°C for 45 sec, and 72°C for 10 min. Cycles 2 through 4 were repeated 30 times.

- The PCR products were separated on a 1% agarose gel and a 500 bp PCR fragment
- 20 was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and sequenced using the T7 DNA Sequenase™ kit (Amsham) and the SP6/T7 primers (Stratagene). Sequence analysis revealed that the PCR fragment was indeed an alternatively spliced form of AI307658 having a continuous open reading frame with similarity to other GPCRs. The completed sequence of this PCR fragment was as follows:

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5'-TCACAATGCTAGGTGTGGTCTGGCTGGTGGCAGTCATCGTAGGATCACCCATGTGGCAC
GTGCAACAACCTTGAGATCAAATATGACTTCCTATATGAAAAGGAACACATCTGCTGCTTAAGA
GTGGACCAGCCCTGTGCACCAGAAGATCTACACCACCTTCATCCTTGTCATCCTCTTCCTCCTGC
CTCTTATGGTGATGCTTATTCTGTACGTAAAAATTGGTTATGAACTTTGGATAAAAGAAAAGAGTT
5 GGGGATGGTTCAGTGCTTCGAACTATTCATGGAAAAGAAATGTCCAAAATAGCCAGGAAGAAG
AAACGAGCTGTCATTATGATGGTGACAGTGGTGGCTCTCTTTGCTGTGTGCTGGGCACCATTC
ATGTTGTCCATATGATGATTGAATACAGTAATTTTGAAAAGGAATATGATGATGTCACAATCAA
GATGATTTTGTCTATCGTGCAAATTATTGGATTTTCCAATCCATCTGTAATCCCATTGTCTATGCA-
3' (SEQ.ID.NO.: 47)

10 Based on the above sequence, two sense oligonucleotide primer sets:

5'-CTGCTTAGAAGAGTGGACCAG-3' (SEQ.ID.NO.: 48; oligo 1),

5'-CTGTGCACCAGAAGATCTACAC-3' (SEQ.ID.NO.: 49; oligo 2) and

two antisense oligonucleotide primer sets:

5'-CAAGGATGAAGGTGGTGTAGA-3' (SEQ.ID.NO.: 50; oligo 3)

15 5'-GTGTAGATCTTCTGGTGCACAGG-3' (SEQ.ID.NO.: 51; oligo 4)

were used for 3'- and 5'-RACE PCR with a human brain Marathon-Ready™ cDNA (Clontech, Cat# 7400-1) as template, according to manufacture's instructions. DNA fragments generated by the RACE PCR were cloned into the pCRII-TOPO™ vector (Invitrogen) and sequenced using the SP6/T7 primers (Stratagene) and some internal primers.

20 The 3' RACE product contained a poly(A) tail and a completed open reading frame ending at a TAA stop codon. The 5' RACE product contained an incomplete 5' end; *i.e.*, the ATG initiation codon was not present.

Based on the new 5' sequence, oligo 3 and the following primer:

5'-GCAATGCAGGTCATAGTGAGC-3' (SEQ.ID.NO.: 52; oligo 5)

25 were used for the second round of 5' race PCR and the PCR products were analyzed as above.

A third round of 5' race PCR was carried out utilizing antisense primers:

5'-TGGAGCATGGTGACGGGAATGCAGAAG-3' (SEQ.ID.NO.: 53; oligo 6) and

5'-GTGATGAGCAGGTCAGCGCCAAG-3' (SEQ.ID.NO.: 54; oligo 7).

The sequence of the 5' RACE PCR products revealed the presence of the initiation codon

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ATG, and further round of 5' race PCR did not generate any more 5' sequence. The completed 5' sequence was confirmed by RT-PCR using sense primer

5'-GCAATGCAGGCGCTTAACATTAC-3' (SEQ.ID.NO.: 55; oligo 8)

and oligo 4 as primers and sequence analysis of the 650 bp PCR product generated from
5 human brain and heart cDNA templates (Clontech, Cat# 7404-1). The completed 3' sequence was confirmed by RT-PCR using oligo 2 and the following antisense primer:

5'-TTGGGTTACAATCTGAAGGGCA-3' (SEQ.ID.NO.:56; oligo 9)

and sequence analysis of the 670 bp PCR product generated from human brain and heart cDNA templates. (Clontech, Cat# 7404-1).

10

d. RUP5

The full length RUP5 was cloned by RT-PCR using a sense primer upstream from ATG, the initiation codon (SEQ.ID.NO.:57), and an antisense primer containing TCA as the stop codon (SEQ.ID.NO.:58), which had the following sequences:

5'-ACTCCGTGTCCAGCAGGACTCTG-3' (SEQ.ID.NO.: 57)

15 5'-TGCGTGTTCTGGACCCTCACGTG-3' (SEQ.ID.NO.: 58)

and human peripheral leukocyte cDNA (Clontech) as a template. Advantage™ cDNA polymerase (Clontech) was used for the amplification in a 50ul reaction by the following cycle with step 2 through step 4 repeated 30 times: 94°C for 30 sec; 94° for 15 sec; 69° for 40 sec; 72°C for 3 min; and 72°C fro 6 min. A 1.4kb PCR fragment was isolated and cloned with
20 the pCRII-TOPO™ vector (Invitrogen) and completely sequenced using the T7 DNA Sequenase™ kit (Amsham). See, SEQ.ID.NO.: 9.

e. RUP6

The full length RUP6 was cloned by RT-PCR using primers:

5'-CAGGCCTTGGATTTTAATGTCAGGGATGG-3' (SEQ.ID.NO.: 59) and

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5'-GGAGAGTCAGCTCTGAAAGAATTCAGG-3' (SEQ.ID.NO.: 60);
and human thymus Marathon-Ready™ cDNA (Clontech) as a template. Advantage cDNA polymerase (Clontech, according to manufacturer's instructions) was used for the amplification in a 50ul reaction by the following cycle: 94°C for 30sec; 94°C for 5 sec; 66°C
5 for 40sec; 72°C for 2.5 sec and 72°C for 7 min. Cycles 2 through 4 were repeated 30 times. A 1.3 Kb PCR fragment was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and completely sequenced (*see*, SEQ.ID.NO.: 11) using the ABI Big Dye Terminator™ kit (P.E. Biosystem).

f. RUP7

10 The full length RUP7 was cloned by RT-PCR using primers:
5'-TGATGTGATGCCAGATACTAATAGCAC-3' (SEQ.ID.NO.: 61; sense) and
5'-CCTGATTCATTTAGGTGAGATTGAGAC-3' (SEQ.ID.NO.: 62; antisense)
and human peripheral leukocyte cDNA (Clontech) as a template. Advantage™ cDNA polymerase (Clontech) was used for the amplification in a 50 ul reaction by the following
15 cycle with step 2 to step 4 repeated 30 times: 94°C for 2 minutes; 94°C for 15 seconds; 60°C for 20 seconds; 72°C for 2 minutes; 72°C for 10 minutes. A 1.25 Kb PCR fragment was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator™ kit (P.E. Biosystem). *See*, SEQ.ID.NO.: 13.

3. Angiotensin II Type 1 Receptor ("AT1")

20 The endogenous human angiotensin II type 1 receptor ("AT1") was obtained by PCR using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 µM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 55°C for 1min and 72°C for 1.5 min. The 5' PCR primer contains a HindIII site with the sequence:

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5'-CCCAAGCTTCCCCAGGTGTATTTGAT-3' (SEQ.ID.NO.: 63)

and the 3' primer contains a BamHI site with the following sequence:

5'-GTTGGATCCACATAATGCATTTTCTC-3' (SEQ.ID.NO.: 64).

The resulting 1.3 kb PCR fragment was digested with HindIII and BamHI and cloned into
5 HindIII-BamHI site of pCMV expression vector. The cDNA clone was fully sequenced.
Nucleic acid (SEQ.ID.NO.: 65) and amino acid (SEQ.ID.NO.: 66) sequences for human AT1
were thereafter determined and verified.

4. GPR38

To obtain GPR38, PCR was performed by combining two PCR fragments, using
10 human genomic cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system
provided by the manufacturer, 0.25uM of each primer, and 0.2 mM of each 4 nucleotides.
The cycle condition for each PCR reaction was 30 cycles of 94°C for 1 min, 62°C for 1min
and 72°C for 2 min.

The first fragment was amplified with the 5' PCR primer that contained an end site
15 with the following sequence:

5'-ACCATGGGCAGCCCCTGGAACGGCAGC-3' (SEQ.ID.NO.:67)

and a 3' primer having the following sequence:

5'-AGAACCACCACCAGCAGGACGCGGACGGTCTGCCGGTGG-3' (SEQ.ID.NO.:68).

The second PCR fragment was amplified with a 5' primer having the following sequence:

20 5'-GTCCGCGTCCTGCTGGTGGTGGTTCTGGCATTATAATT-3' (SEQ.ID.NO.: 69)

and a 3' primer that contained a BamHI site and having the following sequence:

5'-CCTGGATCCTTATCCCATCGTCTTCACGTTAGC-3' (SEQ.ID.NO.: 70).

The two fragments were used as templates to amplify GPR38, using SEQ.ID.NO.: 67 and
SEQ.ID.NO.: 70 as primers (using the above-noted cycle conditions). The resulting 1.44kb

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PCR fragment was digested with BamHI and cloned into Blunt-BamHI site of pCMV expression vector.

5. MC4

To obtain MC4, PCR was performed using human genomic cDNA as template and
5 rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25uM
of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition for each PCR reaction
was 30 cycles of 94°C for 1 min, 54°C for 1min and 72°C for 1.5 min.

The 5' PCR contained an EcoRI site with the sequence:

5'-CTGGAATTCTCTGCCAGCATGGTGA-3' (SEQ.ID.NO.: 71)

10 and the 3' primer contained a BamHI site with the sequence:

5'-GCAGGATCCTATATTGCGTGCTCTGTCCCC'-3 (SEQ.ID.NO.: 72).

The 1.0 kb PCR fragment was digested with EcoRI and BamHI and cloned into EcoRI-BamHI
site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 73) and amino acid
(SEQ.ID.NO.: 74) sequences for human MC4 were thereafter determined.

15 6. CCKB

To obtain CCKB, PCR was performed using human stomach cDNA as template and
rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25uM
of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition for each PCR reaction
was 30 cycles of 94°C for 1 min, 65°C for 1min and 72°C for 1 min and 30 sec.

20 The 5' PCR contained a HindIII site with the sequence:

5'-CCGAAGCTTCGAGCTGAGTAAGGCGGGGCT-3' (SEQ.ID.NO.: 75)

and the 3' primer contained an EcoRI site with the sequence:

5'-GTGGAATTCATTGCCCCTGCCTCAACCCCA-3 (SEQ.ID.NO.: 76).

The resulting 1.44 kb PCR fragment was digested with HindIII and EcoRI and cloned into

HindIII-EcoRI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 77) and amino acid (SEQ.ID.NO.: 78) sequences for human CCKB were thereafter determined.

7. TDAG8

To obtain TDAG8, PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 56°C for 1min and 72 °C for 1 min and 20 sec. The 5' PCR primer contained a HindIII site with the following sequence:

5'-TGCAAGCTTAAAAAGGAAAAAATGAACAGC-3' (SEQ.ID.NO.: 79)

10 and the 3' primer contained a BamHI site with the following sequence:

5'-TAAGGATCCCTTCCCTTCAAAACATCCTTG -3' (SEQ.ID.NO.: 80).

The resulting 1.1 kb PCR fragment was digested with HindIII and BamHI and cloned into HindIII-BamHI site of pCMV expression vector. Three resulting clones sequenced contained three potential polymorphisms involving changes of amino acid 43 from Pro to Ala, amino acid 97 from Lys to Asn and amino acid 130 from Ile to Phe. Nucleic acid (SEQ.ID.NO.: 81) and amino acid (SEQ.ID.NO.: 82) sequences for human TDAG8 were thereafter determined.

8. H9

To obtain H9, PCR was performed using pituitary cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 μ M of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 62°C for 1 min and 72°C for 2 min. The 5' PCR primer contained a HindIII site with the following sequence:

5'-GGAAAGCTTAACGATCCCCAGGAGCAACAT-3' (SEQ.ID.NO.:15)

and the 3' primer contained a BamHI site with the following sequence:

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5'-CTGGGATCCTACGAGAGCATTTTTCACACAG-3' (SEQ.ID.NO.:16).

The resulting 1.9 kb PCR fragment was digested with HindIII and BamHI and cloned into HindIII-BamHI site of pCMV expression vector. H9 contained three potential polymorphisms involving changes of amino acid P320S, S493N and amino acid G448A. Nucleic acid
5 (SEQ.ID.NO.: 139) and amino acid (SEQ.ID.NO.: 140) sequences for human H9 were thereafter determined and verified.

Example 2

PREPARATION OF NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED GPCRS

Those skilled in the art are credited with the ability to select techniques for
10 mutation of a nucleic acid sequence. Presented below are approaches utilized to create non-endogenous versions of several of the human GPCRs disclosed above. The mutations disclosed below are based upon an algorithmic approach whereby the 16th amino acid (located in the IC3 region of the GPCR) from a conserved proline residue (located in the TM6 region of the GPCR, near the TM6/IC3 interface) is mutated, most preferably to a
15 lysine amino acid residue.

1. Transformer Site-Directed TM Mutagenesis

Preparation of non-endogenous human GPCRs may be accomplished on human GPCRs using Transformer Site-DirectedTM Mutagenesis Kit (Clontech) according to the manufacturer instructions. Two mutagenesis primers are utilized, most preferably a lysine
20 mutagenesis oligonucleotide that creates the lysine mutation, and a selection marker oligonucleotide. For convenience, the codon mutation to be incorporated into the human GPCR is also noted, in standard form (Table E):

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TABLE E

	Receptor Identifier	Codon Mutation
	hARE-3	F313K
	hARE-4	V233K
5	hARE-5	A240K
	hGPCR14	L257K
	hGPCR27	C283K
	hARE-1	E232K
	hARE-2	G285K
10	hPPR1	L239K
	hG2A	K232A
	hRUP3	L224K
	hRUP5	A236K
	hRUP6	N267K
15	hRUP7	A302K
	hCHN4	V236K
	hMC4	A244K
	hCHN3	S284K
	hCHN6	L352K
20	hCHN8	N235K
	hCHN9	G223K
	hCHN10	L231K
	hH9	F236K

The following GPCRs were mutated according with the above method using the

25 designated sequence primers (Table F).

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TABLE F

Receptor Identifier	Codon Mutation	Lysine Mutagenesis (SEQ.ID.NO.) 5'-3' orientation, mutation sequence underlined	Selection Marker (SEQ.ID.NO.) 5'-3' orientation
hRUP4	V272K	CAGGAAGAAG <u>AAA</u> CGAGC TGTCATTATGATGGTGACA GTG (83)	CACTGTCACCATCATAATG ACAGCTCGTTTCTTCTTCC TG (84)
hAT1	<i>see below</i>	alternative approach; <i>see below</i>	alternative approach; <i>see below</i>
hGPR38	V297K	GGCCACCGGCAGACCA <u>AA</u> C GCGTCCTGCTG (85)	CTCCTTCGGTCCTCCTATC GTTGTCAGAAAGT (86)
hCCKB	V332K	alternative approach; <i>see below</i>	alternative approach; <i>see below</i>
hTDAG8	I225K	GGAAAAGAAGAGAATCAA <u>AAA</u> ACTACTTGTCAGCATC (87)	CTCCTTCGGTCCTCCTATC GTTGTCAGAAAGT (88)
hH9	F236K	GCTGAGGTTGCAATA <u>AA</u> C TAACCATGTTTGTG (143)	CTCCTTCGGTCCTCCTATC GTTGTCAGAAAGT (144)
hMC4	A244K	GCCAATATGAAGGGA <u>AAA</u> ATTACCTTGACCATC (137)	CTCCTTCGGTCCTCCTATC GTTGTCAGAAAGT (138)

The non-endogenous human GPCRs were then sequenced and the derived and verified nucleic acid and amino acid sequences are listed in the accompanying "Sequence Listing" appendix to this patent document, as summarized in Table G below:

TABLE G

	Non Endogenous Human GPCR	Nucleic Acid Sequence Listing	Amino Acid Sequence Listing
15	hRUP4 (V272K)	SEQ.ID.NO.: 127	SEQ.ID.NO.: 128
20	hAT1 (<i>see alternative approaches below</i>)	(<i>see alternative approaches below</i>)	(<i>see alternative approaches, below</i>)
	hGPR38 (V297K)	SEQ.ID.NO.: 129	SEQ.ID.NO.: 130
25	hCCKB (V332K)	SEQ.ID.NO.: 131	SEQ.ID.NO.: 132
	hTDAG8 (I225K)	SEQ.ID.NO.: 133	SEQ.ID.NO.: 134
	hH9 (F236K)	SEQ.ID.NO.: 141	SEQ.ID.NO.: 142
30	hMC4 (A244K)	SEQ.ID.NO.: 135	SEQ.ID.NO.: 136

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2. Alternative Approaches For Creation of Non-Endogenous Human GPCRs

a. AT1

1. F239K Mutation

Preparation of a non-endogenous, constitutively activated human AT1 receptor was accomplished by creating an F239K mutation (see, SEQ.ID.NO.: 89 for nucleic acid sequence, and SEQ.ID.NO.: 90 for amino acid sequence). Mutagenesis was performed using Transformer Site-Directed Mutagenesis™ Kit (Clontech) according to the to manufacturer's instructions. The two mutagenesis primers were used, a lysine mutagenesis oligonucleotide (SEQ.ID.NO.: 91) and a selection marker oligonucleotide (SEQ.ID.NO.: 92), which had the following sequences:

5'-CCAAGAAATGATGATATTAAGATAATTATGGC-3' (SEQ.ID.NO.: 91)

5'-CTCCTTCGGTCCTCTATCGTTGTCAGAAAGT-3' (SEQ.ID.NO.: 92),

respectively.

2. N111A Mutation

Preparation of a non-endogenous human AT1 receptor was also accomplished by creating an N111A mutation (see, SEQ.ID.NO.:93 for nucleic acid sequence, and SEQ.ID.NO.: 94 for amino acid sequence). Two PCR reactions were performed using pfu polymerase (Stratagene) with the buffer system provided by the manufacturer, supplemented with 10% DMSO, 0.25 µM of each primer, and 0.5 mM of each 4 nucleotides. The 5' PCR sense primer used had the following sequence:

5'-CCCAAGCTTCCCCAGGTGTATTTGAT-3' (SEQ.ID.NO.: 95)

and the antisense primer had the following sequence:

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5'-CCTGCAGGCGAACTGACTCTGGCTGAAG-3' (SEQ.ID.NO.: 96).

The resulting 400 bp PCR fragment was digested with HindIII site and subcloned into HindIII-SmaI site of pCMV vector (5' construct). The 3' PCR sense primer used had the following sequence:

5 5'-CTGTACGCTAGTGTGTTTCTACTCACGTGTCTCAGCATTGAT-3' (SEQ.ID.NO.: 97)

and the antisense primer had the following sequence:.

5'-GTTGGATCCACATAATGCATTTTCTC-3' (SEQ.ID.NO.: 98)

The resulting 880 bp PCR fragment was digested with BamHI and inserted into Pst (blunted by T4 polymerase) and BamHI site of 5' construct to generated the full length

10 N111A construct. The cycle condition was 25 cycles of 94°C for 1 min, 60°C for 1min and 72°C for 1 min (5' PCR) or 1.5 min (3' PCR).

3. AT2K255IC3 Mutation

Preparation of a non-endogenous, constitutively activated human AT1 was accomplished by creating an AT2K255IC3 "domain swap" mutation (see, SEQ.ID.NO.:99

15 for nucleic acid sequence, and SEQ.ID.NO.: 100 for amino acid sequence). Restriction sites flanking IC3 of AT1 were generated to facilitate replacement of the IC3 with corresponding IC3 from angiotensin II type 2 receptor (AT2). This was accomplished by performing two PCR reactions. A 5' PCR fragment (Fragment A) encoded from the 5' untranslated region to the beginning of IC3 was generated by utilizing SEQ.ID.NO.: 63 as
20 sense primer and the following sequence:

5'-TCCGAATTCCAAAATAACTTGTAAGAATGATCAGAAA-3' (SEQ.ID.NO.: 101)

as antisense primer. A 3' PCR fragment (Fragment B) encoding from the end of IC3 to the 3' untranslated region was generated by using the following sequence:

5'-AGATCTTAAGAAGATAATTATGGCAATTGTGCT-3' (SEQ.ID.NO.: 102)

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as sense primer and SEQ.ID.NO.: 64 as antisense primer. The PCR condition was 30 cycles of 94°C for 1 min, 55°C for 1min and 72°C for 1.5 min using endogenous AT1 cDNA clone as template and pfu polymerase (Stratagene), with the buffer systems provided by the manufacturer, supplemented with 10% DMSO, 0.25 µM of each primer, and 0.5 mM of each 4 nucleotides. Fragment A (720 bp) was digested with HindIII and EcoRI and subcloned. Fragment B was digested with BamHI and subcloned into pCMV vector with an EcoRI site 5' to the cloned PCR fragment.

The DNA fragment (Fragment C) encoding IC3 of AT2 with a L255K mutation and containing an EcoRI cohesive end at 5' and a AflII cohesive end at 3', was generated by annealing 2 synthetic oligonucleotides having the following sequences:

5'AATTCGAAAACACTTACTGAAGACGAATAGCTATGGGAAGAACAGGATAACCCGTGACCAA
G-3' (sense; SEQ.ID.NO.: 103)

5'TTAACTTGGTCACGGGTTATCCTGTTCTTCCCATAGCTATTCGTCTTCAGT
AAGTGTTTTTCG-3' (antisense; SEQ.ID.NO.: 104).

Fragment C was inserted in front of Fragment B through EcoRI and AflII site. The resulting clone was then ligated with the Fragment A through the EcoRI site to generate AT1 with AT2K255IC3.

4. A243+ Mutation

Preparation of a non-endogenous human AT1 receptor was also accomplished by creating an A243+ mutation (see, SEQ.ID.NO.: 105 for nucleic acid sequence, and SEQ.ID.NO.: 106 for amino acid sequence). An A243+ mutation was constructed using the following PCR based strategy: Two PCR reactions was performed using pfu polymerase (Stratagene) with the buffer system provided by the manufacturer supplemented with 10% DMSO, 0.25 µM of each primer, and 0.5 mM of each 4 nucleotides. The 5' PCR sense primer

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utilized had the following sequence:

5'-CCCAAGCTTCCCCAGGTGTATTGAT-3' (SEQ.ID.NO.: 107)

and the antisense primer had the following sequence:

5'-AAGCACAATTGCTGCATAATTATCTTAAAAATATCATC-3' (SEQ.ID.NO.: 108).

5 The 3' PCR sense primer utilized had the following sequence:

5'-AAGATAATTATGGCAGCAATTGTGCTTTTCTTTTCTTT-3' (SEQ.ID.NO.: 109)

containing the Ala insertion and antisense primer:

5'-GTTGGATCCACATAATGCATTTTCTC-3' (SEQ.ID.NO.: 110).

The cycle condition was 25 cycles of 94°C for 1 min, 54°C for 1min and 72 °C for 1.5 min.

10 An aliquot of the 5' and 3' PCR were then used as co-template to perform secondary PCR using the 5' PCR sense primer and 3' PCR antisense primer. The PCR condition was the same as primary PCR except the extension time was 2.5 min. The resulting PCR fragment was digested with HindIII and BamHI and subcloned into pCMV vector. (See, SEQ.ID.NO.: 105)

15 4. CCKB

Preparation of the non-endogenous, constitutively activated human CCKB receptor was accomplished by creating a V322K mutation (see, SEQ.ID.NO.: 111 for nucleic acid sequence and SEQ.ID.NO.: 112 for amino acid sequence). Mutagenesis was performed by PCR via amplification using the wildtype CCKB from Example 1.

20 The first PCR fragment (1kb) was amplified by using SEQ.ID.NO.: 75 and an antisense primer comprising a V322K mutation:

5'-CAGCAGCATGCGCTTACGCGCTTCTTAGCCCAG-3' (SEQ.ID.NO.: 113).

The second PCR fragment (0.44kb) was amplified by using a sense primer comprising the V322K mutation:

5'-AGAAGCGCGTGAAGCGCATGCTGCTGGTGATCGTT-3' (SEQ.ID.NO.: 114) and SEQ.ID.NO.:

76.

The two resulting PCR fragments were then used as template for amplifying CCKB comprising V332K, using SEQ.ID.NO.: 75 and SEQ.ID.NO.: 76 and the above-noted
5 system and conditions. The resulting 1.44kb PCR fragment containing the V332K mutation was digested with HindIII and EcoRI and cloned into HindIII-EcoRI site of pCMV expression vector. (See, SEQ.ID.NO.: 111).

3. QuikChange™ Site-Directed™ Mutagenesis

Preparation of non-endogenous human GPCRs can also be accomplished by using
10 QuikChange™ Site-Directed™ Mutagenesis Kit (Stratagene, according to manufacturer's instructions). Endogenous GPCR is preferably used as a template and two mutagenesis primers utilized, as well as, most preferably, a lysine mutagenesis oligonucleotide and a selection marker oligonucleotide (included in kit). For convenience, the codon mutation incorporated into the human GPCR and the respective oligonucleotides are noted, in standard
15 form (Table H):

TABLE H

Receptor Identifier	Codon Mutation	Lysine Mutagenesis (SEQ.ID.NO.) 5'-3' orientation, mutation underlined	Selection Marker (SEQ.ID.NO.) 5'-3' orientation
hCHN3	S284K	ATGGAGAAAAGAATC <u>AAA</u> AGAA TGTTCTATATA (115)	TATATAGAACATTCTTTT GATTCTTTTCTCCAT (116)
hCHN6	L352K	CGCTCTCTGGCCTTG <u>AAG</u> CGCAC GCTCAGC (117)	GCTGAGCGTGCGCTTCA AGGCCAGAGAGCG (118)
5 hCHN8	N235K	CCCAGGAAAAAGGTG <u>AA</u> AGTCA AAGTTTTC (119)	GAAAACTTTGACTTTCAC CTTTTTCCTGGG (120)
hCHN9	G223K	GGGGCGCGGGTG <u>AA</u> ACGGCTGG TGAGC (121)	GCTCACCAGCCGTTTCA CCCGCGCCCC (122)
hCHN10	L231K	CCCCTTG <u>AA</u> AGCCTAAGAACTT GGTCATC (123)	GATGACCAAGTTCCTAG GCTTTCAAGGGG (124)

Example 3**RECEPTOR EXPRESSION**

10 Although a variety of cells are available to the art for the expression of proteins, it is most preferred that mammalian cells be utilized. The primary reason for this is predicated upon practicalities, *i.e.*, utilization of, *e.g.*, yeast cells for the expression of a GPCR, while possible, introduces into the protocol a non-mammalian cell which may not (indeed, in the case of yeast, does not) include the receptor-coupling, genetic-mechanism and secretory

15 pathways that have evolved for mammalian systems – thus, results obtained in non-mammalian cells, while of potential use, are not as preferred as that obtained from mammalian cells. Of the mammalian cells, COS-7, 293 and 293T cells are particularly preferred, although the specific mammalian cell utilized can be predicated upon the particular needs of the artisan.

On day one, 1×10^7 293T cells per 150mm plate were plated out. On day two, two

20 reaction tubes were prepared (the proportions to follow for each tube are per plate): tube A was prepared by mixing 20µg DNA (*e.g.*, pCMV vector; pCMV vector with receptor cDNA, etc.) in 1.2ml serum free DMEM (Irvine Scientific, Irvine, CA); tube B was

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prepared by mixing 120 μ l lipofectamine (Gibco BRL) in 1.2ml serum free DMEM. Tubes A and B were admixed by inversions (several times), followed by incubation at room temperature for 30-45min. The admixture is referred to as the "transfection mixture". Plated 293T cells were washed with 1XPBS, followed by addition of 10ml serum free DMEM. 2.4ml of the transfection mixture were added to the cells, followed by incubation for 4hrs at 37°C/5% CO₂. The transfection mixture was removed by aspiration, followed by the addition of 25ml of DMEM/10% Fetal Bovine Serum. Cells were incubated at 37°C/5% CO₂. After 72hr incubation, cells were harvested and utilized for analysis.

Example 4**10 ASSAYS FOR DETERMINATION OF CONSTITUTIVE ACTIVITY OF NON-ENDOGENOUS GPCRS**

A variety of approaches are available for assessment of constitutive activity of the non-endogenous human GPCRs. The following are illustrative; those of ordinary skill in the art are credited with the ability to determine those techniques that are preferentially beneficial for the needs of the artisan.

1. Membrane Binding Assays: [³⁵S]GTP γ S Assay

When a G protein-coupled receptor is in its active state, either as a result of ligand binding or constitutive activation, the receptor couples to a G protein and stimulates the release of GDP and subsequent binding of GTP to the G protein. The alpha subunit of the G protein-receptor complex acts as a GTPase and slowly hydrolyzes the GTP to GDP, at which point the receptor normally is deactivated. Constitutively activated receptors continue to exchange GDP for GTP. The non-hydrolyzable GTP analog, [³⁵S]GTP γ S, can be utilized to demonstrate enhanced binding of [³⁵S]GTP γ S to membranes expressing constitutively activated receptors. The advantage of using [³⁵S]GTP γ S binding to measure constitutive

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activation is that: (a) it is generically applicable to all G protein-coupled receptors; (b) it is proximal at the membrane surface making it less likely to pick-up molecules which affect the intracellular cascade.

The assay utilizes the ability of G protein coupled receptors to stimulate [³⁵S]GTPγS binding to membranes expressing the relevant receptors. The assay can, therefore, be used in the direct identification method to screen candidate compounds to known, orphan and constitutively activated G protein-coupled receptors. The assay is generic and has application to drug discovery at all G protein-coupled receptors.

The [³⁵S]GTPγS assay can be incubated in 20 mM HEPES and between 1 and about 20mM MgCl₂ (this amount can be adjusted for optimization of results, although 20mM is preferred) pH 7.4, binding buffer with between about 0.3 and about 1.2 nM [³⁵S]GTPγS (this amount can be adjusted for optimization of results, although 1.2 is preferred) and 12.5 to 75 μg membrane protein (*e.g.* COS-7 cells expressing the receptor; this amount can be adjusted for optimization, although 75μg is preferred) and 1 μM GDP (this amount can be changed for optimization) for 1 hour. Wheatgerm agglutinin beads (25 μl; Amersham) should then be added and the mixture incubated for another 30 minutes at room temperature. The tubes are then centrifuged at 1500 x g for 5 minutes at room temperature and then counted in a scintillation counter.

A less costly but equally applicable alternative has been identified which also meets the needs of large scale screening. Flash plates™ and Wallac™ scintistrips may be utilized to format a high throughput [³⁵S]GTPγS binding assay. Furthermore, using this technique, the assay can be utilized for known GPCRs to simultaneously monitor tritiated ligand binding to the receptor at the same time as monitoring the efficacy via [³⁵S]GTPγS binding. This is

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possible because the Wallac beta counter can switch energy windows to look at both tritium and ^{35}S -labeled probes. This assay may also be used to detect other types of membrane activation events resulting in receptor activation. For example, the assay may be used to monitor ^{32}P phosphorylation of a variety of receptors (both G protein coupled and tyrosine kinase receptors). When the membranes are centrifuged to the bottom of the well, the bound ^{35}S GTP γ S or the ^{32}P -phosphorylated receptor will activate the scintillant which is coated of the wells. Scinti $^{\circ}$ strips (Wallac) have been used to demonstrate this principle. In addition, the assay also has utility for measuring ligand binding to receptors using radioactively labeled ligands. In a similar manner, when the radiolabeled bound ligand is centrifuged to the bottom of the well, the scintistrip label comes into proximity with the radiolabeled ligand resulting in activation and detection.

2. Adenylyl Cyclase

A Flash Plate $^{\text{TM}}$ Adenylyl Cyclase kit (New England Nuclear; Cat. No. SMP004A) designed for cell-based assays can be modified for use with crude plasma membranes. The Flash Plate wells contain a scintillant coating which also contains a specific antibody recognizing cAMP. The cAMP generated in the wells was quantitated by a direct competition for binding of radioactive cAMP tracer to the cAMP antibody. The following serves as a brief protocol for the measurement of changes in cAMP levels in membranes that express the receptors.

Transfected cells are harvested approximately three days after transfection. Membranes were prepared by homogenization of suspended cells in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl_2 . Homogenization is performed on ice using a Brinkman Polytron $^{\text{TM}}$ for approximately 10 seconds. The resulting homogenate is centrifuged at 49,000

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X g for 15 minutes at 4°C. The resulting pellet is then resuspended in buffer containing 20mM HEPES, pH 7.4 and 0.1 mM EDTA, homogenized for 10 seconds, followed by centrifugation at 49,000 X g for 15 minutes at 4°C. The resulting pellet can be stored at -80°C until utilized. On the day of measurement, the membrane pellet is slowly thawed at room temperature, resuspended in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl₂ (these amounts can be optimized, although the values listed herein are preferred), to yield a final protein concentration of 0.60mg/ml (the resuspended membranes were placed on ice until use).

cAMP standards and Detection Buffer (comprising 2 µCi of tracer [¹²⁵I] cAMP (100 µl] to 11 ml Detection Buffer) are prepared and maintained in accordance with the manufacturer's instructions. Assay Buffer is prepared fresh for screening and contained 20mM HEPES, pH 7.4, 10mM MgCl₂, 20mM (Sigma), 0.1 units/ml creatine phosphokinase (Sigma), 50 µM GTP (Sigma), and 0.2 mM ATP (Sigma); Assay Buffer can be stored on ice until utilized. The assay is initiated by addition of 50ul of assay buffer followed by addition of 50ul of membrane suspension to the NEN Flash Plate. The resultant assay mixture is incubated for 60 minutes at room temperature followed by addition of 100ul of detection buffer. Plates are then incubated an additional 2-4 hours followed by counting in a Wallac MicroBeta™ scintillation counter. Values of cAMP/well are extrapolated from a standard cAMP curve that is contained within each assay plate.

20 C. Reporter-Based Assays

1. CREB Reporter Assay (Gs-associated receptors)

A method to detect Gs stimulation depends on the known property of the transcription factor CREB, which is activated in a cAMP-dependent manner. A PathDetect™ CREB trans-

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Reporting System (Stratagene, Catalogue # 219010) can utilized to assay for Gs coupled activity in 293 or 293T cells. Cells are transfected with the plasmids components of this above system and the indicated expression plasmid encoding endogenous or mutant receptor using a Mammalian Transfection Kit (Stratagene, Catalogue #200285) according to the manufacturer's instructions. Briefly, 400 ng pFR-Luc (luciferase reporter plasmid containing Gal4 recognition sequences), 40 ng pFA2-CREB (Gal4-CREB fusion protein containing the Gal4 DNA-binding domain), 80 ng pCMV-receptor expression plasmid (comprising the receptor) and 20 ng CMV-SEAP (secreted alkaline phosphatase expression plasmid; alkaline phosphatase activity is measured in the media of transfected cells to control for variations in transfection efficiency between samples) are combined in a calcium phosphate precipitate as per the Kit's instructions. Half of the precipitate is equally distributed over 3 wells in a 96-well plate, kept on the cells overnight, and replaced with fresh medium the following morning. Forty-eight (48) hr after the start of the transfection, cells are treated and assayed for, e.g., luciferase activity

2. AP1 reporter assay (Gq-associated receptors)

A method to detect Gq stimulation depends on the known property of Gq-dependent phospholipase C to cause the activation of genes containing AP1 elements in their promoter. A Pathdetect™ AP-1 cis-Reporting System (Stratagene, Catalogue # 219073) can be utilized following the protocol set forth above with respect to the CREB reporter assay. except that the components of the calcium phosphate precipitate were 410 ng pAP1-Luc. 80 ng pCMV-receptor expression plasmid, and 20 ng CMV-SEAP.

3. CRE-LUC Reporter Assay

293 and 293T cells are plated-out on 96 well plates at a density of 2×10^4 cells per

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well and were transfected using Lipofectamine Reagent (BRL) the following day according to manufacturer instructions. A DNA/lipid mixture is prepared for each 6-well transfection as follows: 260ng of plasmid DNA in 100 μ l of DMEM were gently mixed with 2 μ l of lipid in 100 μ l of DMEM (the 260ng of plasmid DNA consisted of 200ng of a 8xCRE-Luc reporter plasmid (*see* below and Figure 1 for a representation of a portion of the plasmid), 50ng of pCMV comprising endogenous receptor or non-endogenous receptor or pCMV alone, and 10ng of a GPRS expression plasmid (GPRS in pcDNA3 (Invitrogen)). The 8XCRE-Luc reporter plasmid was prepared as follows: vector SRIF- β -gal was obtained by cloning the rat somatostatin promoter (-71/+51) at BglV-HindIII site in the p β gal-Basic Vector (Clontech).

10 Eight (8) copies of cAMP response element were obtained by PCR from an adenovirus template AdpCF126CCRE8 (*see, 7 Human Gene Therapy* 1883 (1996)) and cloned into the SRIF- β -gal vector at the Kpn-BglV site, resulting in the 8xCRE- β -gal reporter vector. The 8xCRE-Luc reporter plasmid was generated by replacing the beta-galactosidase gene in the 8xCRE- β -gal reporter vector with the luciferase gene obtained from the pGL3-basic vector

15 (Promega) at the HindIII-BamHI site. Following 30 min. incubation at room temperature, the DNA/lipid mixture was diluted with 400 μ l of DMEM and 100 μ l of the diluted mixture was added to each well. 100 μ l of DMEM with 10% FCS were added to each well after a 4hr incubation in a cell culture incubator. The following day the transfected cells were changed with 200 μ l/well of DMEM with 10% FCS. Eight (8) hours later, the wells were changed to

20 100 μ l /well of DMEM without phenol red, after one wash with PBS. Luciferase activity were measured the next day using the LucLite™ reporter gene assay kit (Packard) following manufacturer instructions and read on a 1450 MicroBeta™ scintillation and luminescence counter (Wallac).

4. SRF-LUC Reporter Assay

One method to detect Gq stimulation depends on the known property of Gq-dependent phospholipase C to cause the activation of genes containing serum response factors in their promoter. A Pathdetect™ SRF-Luc-Reporting System (Stratagene) can be utilized to assay
5 for Gq coupled activity in, *e.g.*, COS7 cells. Cells are transfected with the plasmid components of the system and the indicated expression plasmid encoding endogenous or non-endogenous GPCR using a Mammalian Transfection™ Kit (Stratagene, Catalogue #200285) according to the manufacturer's instructions. Briefly, 410 ng SRF-Luc, 80 ng pCMV-receptor expression plasmid and 20 ng CMV-SEAP (secreted alkaline phosphatase expression plasmid;
10 alkaline phosphatase activity is measured in the media of transfected cells to control for variations in transfection efficiency between samples) are combined in a calcium phosphate precipitate as per the manufacturer's instructions. Half of the precipitate is equally distributed over 3 wells in a 96-well plate, kept on the cells in a serum free media for 24 hours. The last 5 hours the cells are incubated with 1 μ M Angiotensin, where indicated. Cells are then lysed
15 and assayed for luciferase activity using a Lucite™ Kit (Packard, Cat. # 6016911) and "Trilux 1450 Microbeta" liquid scintillation and luminescence counter (Wallac) as per the manufacturer's instructions. The data can be analyzed using GraphPad Prism™ 2.0a (GraphPad Software Inc.).

5. Intracellular IP₃ Accumulation Assay

20 On day 1, cells comprising the receptors (endogenous and/or non-endogenous) can be plated onto 24 well plates, usually 1×10^4 cells/well (although this number can be optimized. On day 2 cells can be transfected by firstly mixing 0.25 μ g DNA in 50 μ l serum free DMEM/well and 2 μ l lipofectamine in 50 μ l serumfree DMEM/well. The solutions

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are gently mixed and incubated for 15-30 min at room temperature. Cells are washed with 0.5 ml PBS and 400 μ l of serum free media is mixed with the transfection media and added to the cells. The cells are then incubated for 3-4 hrs at 37°C/5%CO₂ and then the transfection media is removed and replaced with 1ml/well of regular growth media. On

5 day 3 the cells are labeled with ³H-myo-inositol. Briefly, the media is removed and the cells are washed with 0.5 ml PBS. Then 0.5 ml inositol-free/serum free media (GIBCO BRL) is added/well with 0.25 μ Ci of ³H-myo-inositol / well and the cells are incubated for 16-18 hrs o/n at 37°C/5%CO₂. On Day 4 the cells are washed with 0.5 ml PBS and 0.45 ml of assay medium is added containing inositol-free/serum free media 10 μ M pargyline

10 10 mM lithium chloride or 0.4 ml of assay medium and 50 μ l of 10x ketanserin (ket) to final concentration of 10 μ M. The cells are then incubated for 30 min at 37°C. The cells are then washed with 0.5 ml PBS and 200 μ l of fresh/icecold stop solution (1M KOH; 18 mM Na-borate; 3.8 mM EDTA) is added/well. The solution is kept on ice for 5-10 min or until cells were lysed and then neutralized by 200 μ l of fresh/ice cold neutralization sol.

15 (7.5 % HCL). The lysate is then transferred into 1.5 ml eppendorf tubes and 1 ml of chloroform/methanol (1:2) is added/tube. The solution is vortexed for 15 sec and the upper phase is applied to a Biorad AG1-X8™ anion exchange resin (100-200 mesh). Firstly, the resin is washed with water at 1:1.25 W/V and 0.9 ml of upper phase is loaded onto the column. The column is washed with 10 mls of 5 mM myo-inositol and 10 ml of 5

20 mM Na-borate/60mM Na-formate. The inositol tris phosphates are eluted into scintillation vials containing 10 ml of scintillation cocktail with 2 ml of 0.1 M formic acid/ 1 M ammonium formate. The columns are regenerated by washing with 10 ml of 0.1 M formic acid/3M ammonium formate and rinsed twice with dd H₂O and stored at 4°C in water.

Exemplary results are presented below in Table I:

TABLE I

Receptor	Mutation	Assay Utilized	Signal Generated: Endogenous Version (Relative Light Units)	Signal Generated: Non-Endogenous Version (Relative Light Units)	Percent Difference
hAT1	F239K	SRF-LUC	34	137	75% ¹
	AT2K255IC3	SRF-LUC	34	127	73% ¹
5 hTDAG8	I225K	CRE-LUC (293 cells)	2,715	14,440	81% ¹
	I225K	CRE-LUC (293T cells)	65,681	185,636	65% ¹
hH9 hCCKB	F236K	CRE-LUC	1,887	6,096	69% ¹
	V332K	CRE-LUC	785	3,223	76% ¹

C. CELL-BASED DETECTION ASSAY (EXAMPLE -TDAG8)

10 293 cells were plated-out on 150mm plates at a density of 1.3×10^7 cells per plate, and were transfected using 12ug of the respective DNA and 60ul of Lipofectamine Reagent (BRL) per plate. The transfected cells were grown in media containing serum for an assay performed 24 hours post-transfection. For detection assay performed 48 hours post-transfection (assay comparing serum and serum-free media; see Figure 3), the initial media

15 was changed to either serum or serum-free media. The serum-free media was comprised solely of Dulbecco's Modified Eagle's (DME) High Glucose Medium (Irvine Scientific #9024). In addition to the above DME Medium, the media with serum contained the following: 10% Fetal Bovine Serum (Hyclone #SH30071.03), 1% of 100mM Sodium Pyruvate (Irvine Scientific #9334), 1% of 20mM L-Glutamine (Irvine Scientific #9317), and 1% of Penicillin-

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Streptomycin solution (Irvine Scientific #9366).

A 96-well Adenylyl Cyclase Activation Flashplate™ was used (NEN: #SMP004A). First, 50ul of the standards for the assay were added to the plate, in duplicate, ranging from concentrations of 50pmol to zero pmol cAMP per well. The standard cAMP (NEN: #SMP004A) was reconstituted in water, and serial dilutions were made using 1xPBS (Irvine Scientific: #9240). Next, 50ul of the stimulation buffer (NEN: #SMP004A) was added to all wells. In the case of using compounds to measure activation or inactivation of cAMP, 10ul of each compound, diluted in water, was added to its respective well, in triplicate. Various final concentrations used range from 1uM up to 1mM. Adenosine 5'-triphosphate, ATP, (Research Biochemicals International: #A-141) and Adenosine 5'-diphosphate, ADP, (Sigma: #A2754) were used in the assay. Next, the 293 cells transfected with the respective cDNA (CMV or TDAG8) were harvested 24 (assay detection in serum media) or 48 hours post-transfection (assay detection comparing serum and serum-free media). The media was aspirated and the cells washed once with 1xPBS. Then 5ml of 1xPBS was added to the cells along with 3ml of cell dissociation buffer (Sigma: #C-1544). The detached cells were transferred to a centrifuge tube and centrifuged at room temperature for five minutes. The supernatant was removed and the cell pellet was resuspended in an appropriate amount of 1xPBS to obtain a final concentration of 2×10^6 cells per milliliter. To the wells containing the compound, 50ul of the cells in 1xPBS (1×10^5 cells/well) were added. The plate was incubated on a shaker for 15 minutes at room temperature. The detection buffer containing the tracer cAMP was prepared. In 1 ml of detection buffer (NEN: #SMP004A), 50ul (equal to 1uCi) of [125 I]cAMP (NEN: #SMP004A) was added. Following incubation, 50ul of this detection-buffer containing tracer cAMP was added to each well. The plate was placed on a shaker and

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incubated at room temperature for two hours. Finally, the solution from the wells of the plate were aspirated and the flashplate was counted using the Wallac MicroBeta™ scintillation counter.

In Figure 2A, ATP and ADP bind to endogenous TDAG8 resulting in an increase of cAMP of about 59% and about 55% respectively. Figure 2B evidences ATP and ADP binding to endogenous TDAG8 where endogenous TDAG8 was transfected and grown in serum and serum-free medium. ATP binding to endogenous TDAG8 grown in serum media evidences an increase in cAMP of about 65%, compared to the endogenous TDAG8 with no compounds; in serum-free media there was an increase of about 68%. ADP binding to endogenous TDAG8 in serum evidences about a 61% increase, while in serum-free ADP binding evidences an increase of about 62% increase. ATP and ADP bind to endogenous TDAG8 with an EC50 value of 139.8uM and 120.5uM, respectively (data not shown).

Although the results presented in Figure 2B indicate substantially the same results when serum and serum-free media were compared, our choice is to use a serum based media, although a serum-free media can also be utilized.

Example 6

GPCR FUSION PROTEIN PREPARATION

The design of the constitutively activated GPCR-G protein fusion construct was accomplished as follows: both the 5' and 3' ends of the rat G protein Gs α (long form; Itoh, H. et al., 83 *PNAS* 3776 (1986)) were engineered to include a HindIII (5'-AAGCTT-3') sequence thereon. Following confirmation of the correct sequence (including the flanking HindIII sequences), the entire sequence was shuttled into pcDNA3.1(-) (Invitrogen, cat. no. V795-20) by subcloning using the HindIII restriction site of that vector. The correct

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orientation for the Gs α sequence was determined after subcloning into pcDNA3.1(-). The modified pcDNA3.1(-) containing the rat Gs α gene at HindIII sequence was then verified; this vector was now available as a "universal" Gs α protein vector. The pcDNA3.1(-) vector contains a variety of well-known restriction sites upstream of the HindIII site, thus
5 beneficially providing the ability to insert, upstream of the Gs protein, the coding sequence of an endogenous, constitutively active GPCR. This same approach can be utilized to create other "universal" G protein vectors, and, of course, other commercially available or proprietary vectors known to the artisan can be utilized – the important criteria is that the sequence for the GPCR be upstream and in-frame with that of the G protein.

10 TDAG8 couples via Gs, while H9 couples via Gz. For the following exemplary GPCR Fusion Proteins, fusion to Gs α was accomplished.

A TDAG8(I225K)-Gs α Fusion Protein construct was made as follows: primers were designed as follows:

5'-gatcTCTAGAATGAACAGCACATGTATTGAAG-3' (SEQ.ID.NO.: 125; sense)

15 5'-ctagGGTACCCGCTCAAGGACCTCTAATTCCATAG-3' (SEQ.ID.NO.: 126; antisense).

Nucleotides in lower caps are included as spacers in the restriction sites between the G protein and TDAG8. The sense and anti-sense primers included the restriction sites for XbaI and KpnI, respectively.

PCR was then utilized to secure the respective receptor sequences for fusion within
20 the Gs α universal vector disclosed above, using the following protocol for each: 100ng cDNA for TDAG8 was added to separate tubes containing 2ul of each primer (sense and anti-sense), 3uL of 10mM dNTPs, 10uL of 10XTaqPlus™ Precision buffer, 1uL of TaqPlus™ Precision polymerase (Stratagene: #600211), and 80uL of water. Reaction temperatures and cycle times for TDAG8 were as follows: the initial denaturing step was done at 94°C for five minutes, and

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a cycle of 94°C for 30 seconds; 55°C for 30 seconds; 72°C for two minutes. A final extension time was done at 72°C for ten minutes. PCR product for was run on a 1% agarose gel and then purified (data not shown). The purified product was digested with XbaI and KpnI (New England Biolabs) and the desired inserts purified and ligated into the Gs universal
5 vector at the respective restriction site. The positive clones was isolated following transformation and determined by restriction enzyme digest; expression using 293 cells was accomplished following the protocol set forth *infra*. Each positive clone for TDAG8:Gs - Fusion Protein was sequenced to verify correctness.

GPCR Fusion Proteins comprising non-endogenous, constitutively activated
10 TDAG8(I225K) were analyzed as above and verified for constitutive activation.

An H9(F236K)-Gsa Fusion Protein construct was made as follows: primers were designed as follows:

5'-TTAgatcGGGGCCCAACCTAGCGGT-3' (SEQ.ID.NO.: 145; sense)

5'-ggtagcCCCACAGCCATTTCATCAGGATC-3' (SEQ.ID.NO.: 146; antisense).

15 Nucleotides in lower caps are included as spacers in the restriction sites between the G protein and H9. The sense and anti-sense primers included the restriction sites for EcoRV and KpnI, respectively such that spacers (attributed to the restriction sites) exists between the G protein and H9.

PCR was then utilized to secure the respective receptor sequences for fusion within
20 the Gsa universal vector disclosed above, using the following protocol for each: 80ng cDNA for H9 was added to separate tubes containing 100ng of each primer (sense and anti-sense), and 45uL of PCR Supermix™ (Gibco-Brl, LifeTech) (50ul total reaction volume). Reaction temperatures and cycle times for H9 were as follows: the initial denaturing step was done at 94°C for one, and a cycle of 94°C for 30 seconds; 55°C for 30 seconds; 72°C for two

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minutes. A final extension time was done at 72°C for seven minutes. PCR product for was run on a 1% agarose gel and then purified (data not shown). The purified product was cloned into pCRII-TOPO™ System followed by identification of positive clones. Positive clones were isolated, digested with EcoRV and KpnI (New England Biolabs) and the desired inserts were isolated, purified and ligated into the Gs universal vector at the respective restriction site.

The positive clones was isolated following transformation and determined by restriction enzyme digest; expression using 293 cells was accomplished following the protocol set forth *infra*. Each positive clone for H9(F236K):Gs - Fusion Protein was sequenced to verify correctness. Membranes were frozen (-80°C) until utilized.

To ascertain the ability of measuring a cAMP response mediated by the Gs protein (even though H9 couples with Gz), the following cAMP membrane assay was utilized, based upon an NEN Adenyl Cyclase Activation Flahplate™ Assay kit (96 well format). "Binding Buffer" consisted of 10mM HEPES, 100mM NaCl and 10mM MgCl (ph 7.4). "Regeneration Buffer" was prepared in Binding Buffer and consisted of 20mM phosphocreatine, 20U creatine phosphokinase, 20uM GTP, 0.2mM ATP, and 0.6mM IBMX. "cAMP Standards" were prepared in Binding Buffer as follows:

	cAMP Stock (5,000 pmol/ml in 2ml H ₂ O) in ul		Added to indicted amount of Binding Buffer	Final Assay Concentration (50ul into 100ul) to achieve indicated pmol/well
20	A	250	1ml	50
	B	500 of A	500ul	25
	C	500 of B	500ul	12.5
	D	500 of C	750ul	5.0
	E	500 of D	500ul	2.5
25	F	500 of E	500ul	1.25
	G	500 of F	750ul	0.5

Frozen membranes (both pCMV as control and the non-endogenous H(-Gs Fusion Protein) were thawed (on ice at room temperature until in solution). Membranes were

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homogenized with a polytron until in suspension (2 x 15 seconds). Membrane protein concentration was determined using the Bradford Assay Protocol (*see infra*). Membrane concentration was diluted to 0.5mg/ml in Regeneration Buffer (final assay concentration - 25ug/well). Thereafter, 50ul of Binding Buffer was added to each well. For control, 50ul/well of cAMP standard was added to wells 11 and 12 A-G, with Binding Buffer alone to 12H (on the 96-well format). Thereafter, 50ul/well of protein was added to the wells and incubated at room temperature (on shaker) for 60min. 100ul [¹²⁵I]cAMP in Detection Buffer (*see infra*) was added to each well (final - 50ul [¹²⁵I]cAMP into 11ml Detection Buffer). These were incubated for 2hrs at room temperature. Plates were aspirated with an 8 channel manifold and sealed with plate covers. Results (pmoles cAMP bound) were read in a Wallac™ 1450 on "prot #15). Results are presented in Figure 3.

The results presented in Figure 3 indicate that the Gs coupled fusion was able to "drive" the cyclase reaction such that measurement of the constitutive activation of H9(F236K) was viable. Based upon these results, the direct identification of candidate compounds that are inverse agonists, agonists and partial agonists is possible using a cyclase-based assay.

Example 6

Protocol: Direct Identification of Inverse Agonists and Agonists Using [³⁵S]GTPγS

Although we have utilized endogenous, constitutively active GPCRs for the direct identification of candidate compounds as, e.g., inverse agonists, for reasons that are not altogether understood, intra-assay variation can become exacerbated. Preferably, then, a GPCR Fusion Protein, as disclosed above, is also utilized with a non-endogenous, constitutively activated GPCR. We have determined that when such a protein is used, intra-assay variation appears to be substantially stabilized, whereby an effective signal-to-noise ratio is obtained. This has the beneficial result of allowing for a more robust identification

of candidate compounds. Thus, it is preferred that for direct identification, a GPCR Fusion Protein be used and that when utilized, the following assay protocols be utilized.

Membrane Preparation

Membranes comprising the non-endogenous, constitutively active orphan GPCR Fusion Protein of interest and for use in the direct identification of candidate compounds as inverse agonists, agonists or partial agonists are preferably prepared as follows:

a. Materials

"Membrane Scrape Buffer" is comprised of 20mM HEPES and 10mM EDTA, pH 7.4;

"Membrane Wash Buffer" is comprised of 20 mM HEPES and 0.1 mM EDTA, pH 7.4;

10 "Binding Buffer" is comprised of 20mM HEPES, 100 mM NaCl, and 10 mM MgCl₂, pH 7.4

b. Procedure

All materials are kept on ice throughout the procedure. Firstly, the media is aspirated from a confluent monolayer of cells, followed by rinse with 10ml cold PBS, followed by aspiration. Thereafter, 5ml of Membrane Scrape Buffer is added to scrape cells; this is followed by transfer of cellular extract into 50ml centrifuge tubes (centrifuged at 20,000 rpm for 17 minutes at 4°C). Thereafter, the supernatant is aspirated and the pellet is resuspended in 30ml Membrane Wash Buffer followed by centrifuge at 20,000 rpm for 17 minutes at 4°C. The supernatant is then aspirated and the pellet resuspended in Binding Buffer. This is then homogenized using a Brinkman polytron™ homogenizer (15-20 second bursts until the all material is in suspension). This is referred to herein as "Membrane Protein".

Bradford Protein Assay

Following the homogenization, protein concentration of the membranes is determined using the Bradford Protein Assay (protein can be diluted to about 1.5mg/ml, aliquoted and

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frozen (-80°C) for later use; when frozen, protocol for use is as follows: on the day of the assay, frozen Membrane Protein is thawed at room temperature, followed by vortex and then homogenized with a polytron at about 12 x 1,000 rpm for about 5-10 seconds; it is noted that for multiple preparations, the homogenizer should be thoroughly cleaned between
5 homogenization of different preparations).

a. Materials

Binding Buffer (as per above); Bradford Dye Reagent; Bradford Protein Standard are utilized, following manufacturer instructions (Biorad, cat. no. 500-0006).

b. Procedure

10 Duplicate tubes are prepared, one including the membrane, and one as a control "blank". Each contained 800ul Binding Buffer. Thereafter, 10ul of Bradford Protein Standard (1mg/ml) is added to each tube, and 10ul of membrane Protein is then added to just one tube (not the blank). Thereafter, 200ul of Bradford Dye Reagent is added to each tube, followed by vortex of each. After five (5) minutes, the tubes were re-vortexed and the material therein
15 is transferred to cuvettes. The cuvettes are then read using a CECIL 3041 spectrophotometer, at wavelength 595.

Direct Identification Assay

a. Materials

GDP Buffer consists of 37.5 ml Binding Buffer and 2mg GDP (Sigma, cat. no. G-
20 7127), followed by a series of dilutions in Binding Buffer to obtain 0.2 uM GDP (final concentration of GDP in each well was 0.1 uM GDP); each well comprising a candidate compound, has a final volume of 200ul consisting of 100ul GDP Buffer (final concentration, 0.1uM GDP), 50ul Membrane Protein in Binding Buffer, and 50ul [³⁵S]GTPγS (0.6 nM) in

Binding Buffer (2.5 ul [³⁵S]GTPγS per 10ml Binding Buffer).

b. Procedure

Candidate compounds are preferably screened using a 96-well plate format (these can be frozen at -80°C). Membrane Protein (or membranes with expression vector excluding the GPCR Fusion Protein, as control), are homogenized briefly until in suspension. Protein concentration is then determined using the Bradford Protein Assay set forth above. Membrane Protein (and control) is then diluted to 0.25mg/ml in Binding Buffer (final assay concentration, 12.5ug/well). Thereafter, 100 ul GDP Buffer is added to each well of a Wallac Scintistrip™ (Wallac). A 5ul pin-tool is then used to transfer 5 ul of a candidate compound into such well (*i.e.*, 5ul in total assay volume of 200 ul is a 1:40 ratio such that the final screening concentration of the candidate compound is 10uM). Again, to avoid contamination, after each transfer step the pin tool should be rinsed in three reservoirs comprising water (1X), ethanol (1X) and water (2X) – excess liquid should be shaken from the tool after each rinse and dried with paper and kimwipes. Thereafter, 50 ul of Membrane Protein is added to each well (a control well comprising membranes without the GPCR Fusion Protein is also utilized), and pre-incubated for 5-10 minutes at room temperature. Thereafter, 50 ul of [³⁵S]GTPγS (0.6 nM) in Binding Buffer is added to each well, followed by incubation on a shaker for 60 minutes at room temperature (again, in this example, plates were covered with foil). The assay is then stopped by spinning of the plates at 4000 RPM for 15 minutes at 22°C. The plates are then aspirated with an 8 channel manifold and sealed with plate covers. The plates are then read on a Wallac 1450 using setting "Prot. #37" (as per manufacturer instructions).

Example 7

Protocol: Confirmation Assay

Using an independent assay approach to provide confirmation of a directly identified

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candidate compound as set forth above, it is preferred that a confirmation assay then be utilized. In this case, the preferred confirmation assay is a cyclase-based assay.

A modified Flash Plate™ Adenylyl Cyclase kit (New England Nuclear; Cat. No. SMP004A) is preferably utilized for confirmation of candidate compounds directly identified
5 as inverse agonists and agonists to non-endogenous, constitutively activated orphan GPCRs in accordance with the following protocol.

Transfected cells are harvested approximately three days after transfection. Membranes are prepared by homogenization of suspended cells in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl₂. Homogenization is performed on ice using a Brinkman
10 Polytron™ for approximately 10 seconds. The resulting homogenate is centrifuged at 49,000 X g for 15 minutes at 4°C. The resulting pellet is then resuspended in buffer containing 20mM HEPES, pH 7.4 and 0.1 mM EDTA, homogenized for 10 seconds, followed by centrifugation at 49,000 X g for 15 minutes at 4°C. The resulting pellet can be stored at -80°C until utilized. On the day of direct identification screening, the membrane pellet is
15 slowly thawed at room temperature, resuspended in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCL2, to yield a final protein concentration of 0.60mg/ml (the resuspended membranes are placed on ice until use).

cAMP standards and Detection Buffer (comprising 2 μCi of tracer [¹²⁵I cAMP (100 μl) to 11 ml Detection Buffer) are prepared and maintained in accordance with the
20 manufacturer's instructions. Assay Buffer is prepared fresh for screening and contained 20mM HEPES, pH 7.4, 10mM MgCl₂, 20mM phosphocreatine (Sigma), 0.1 units/ml creatine phosphokinase (Sigma), 50 μM GTP (Sigma), and 0.2 mM ATP (Sigma); Assay Buffer can be stored on ice until utilized.

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Candidate compounds identified as per above (if frozen, thawed at room temperature) are added, preferably, to 96-well plate wells ($3\mu\text{l}$ /well; $12\mu\text{M}$ final assay concentration), together with $40\mu\text{l}$ Membrane Protein ($30\mu\text{g}$ /well) and $50\mu\text{l}$ of Assay Buffer. This admixture is then incubated for 30 minutes at room temperature, with gentle shaking.

5 Following the incubation, $100\mu\text{l}$ of Detection Buffer is added to each well, followed by incubation for 2-24 hours. Plates are then counted in a Wallac MicroBeta™ plate reader using "Prot. #31" (as per manufacturer instructions).

It is intended that each of the patents, applications, and printed publications mentioned in this patent document be hereby incorporated by reference in their entirety.

10 As those skilled in the art will appreciate, numerous changes and modifications may be made to the preferred embodiments of the invention without departing from the spirit of the invention. It is intended that all such variations fall within the scope of the invention.

Although a variety of expression vectors are available to those in the art, for purposes of utilization for both the endogenous and non-endogenous human GPCRs, it is
15 most preferred that the vector utilized be pCMV. This vector was deposited with the American Type Culture Collection (ATCC) on October 13, 1998 (10801 University Blvd., Manassas, VA 20110-2209 USA) under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure. The DNA was tested by the ATCC and determined to be. The ATCC has
20 assigned the following deposit number to pCMV: ATCC #203351.

CLAIMS

What is claimed is:

1. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-3(F313K).
- 5 2. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 1.
3. A Plasmid comprising a Vector and the cDNA of claim 1.
4. A Host Cell comprising the Plasmid of claim 3.
5. A cDNA encoding a non-endogenous, constitutively activated version of a human
10 G protein-coupled receptor comprising hARE-4(V233K)
6. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 5.
7. A Plasmid comprising a Vector and the cDNA of claim 5.
8. A Host Cell comprising the Plasmid of claim 7.
- 15 9. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-5(A240K).
10. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 9.
11. A Plasmid comprising a Vector and the cDNA of claim 5.
- 20 12. A Host Cell comprising the Plasmid of claim 11.
13. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hGPCR14(L257K).

14. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 13.
15. A Plasmid comprising a Vector and the cDNA of claim 13.
- 5 16. A Host Cell comprising the Plasmid of claim 15.
17. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hGPCR27(C283K).
18. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 17.
- 10 19. A Plasmid comprising a Vector and the cDNA of claim 17.
20. A Host Cell comprising the Plasmid of claim 19.
21. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-1(E232K).
22. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 21.
- 15 23. A Plasmid comprising a Vector and the cDNA of claim 21.
24. A Host Cell comprising the Plasmid of claim 23.
25. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-2(G285K).
- 20 26. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 25.
27. A Plasmid comprising a Vector and the cDNA of claim 25.
28. A Host Cell comprising the Plasmid of claim 27.

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29. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hPPR1(L239K).
30. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 29.
- 5 31. A Plasmid comprising a Vector and the cDNA of claim 29.
32. A Host Cell comprising the Plasmid of claim 31.
33. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hG2A(K232A).
34. A non-endogenous version of a human G protein-coupled receptor encoded by the
10 cDNA of claim 33.
35. A Plasmid comprising a Vector and the cDNA of claim 33.
36. A Host Cell comprising the Plasmid of claim 35.
37. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hRUP3(L224K).
- 15 38. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 37.
39. A Plasmid comprising a Vector and the cDNA of claim 37.
40. A Host Cell comprising the Plasmid of claim 39.
41. A cDNA encoding a non-endogenous, constitutively activated version of a human
20 G protein-coupled receptor comprising hRUP5(A236K).
42. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 41.
43. A Plasmid comprising a Vector and the cDNA of claim 41.

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44. A Host Cell comprising the Plasmid of claim 42.
45. A cDNA encoding a non-endogenous, constitutively activated version of a human
G protein-coupled receptor comprising hRUP6(N267K)
46. A non-endogenous version of a human G protein-coupled receptor encoded by the
5 cDNA of claim 45.
47. A Plasmid comprising a Vector and the cDNA of claim 45.
48. A Host Cell comprising the Plasmid of claim 47.
49. A cDNA encoding a non-endogenous, constitutively activated version of a human
G protein-coupled receptor comprising hRUP7(A302K).
- 10 50. A non-endogenous version of a human G protein-coupled receptor encoded by the
cDNA of claim 49.
51. A Plasmid comprising a Vector and the cDNA of claim 49.
52. A Host Cell comprising the Plasmid of claim 51.
53. A cDNA encoding a non-endogenous, constitutively activated version of a human
15 G protein-coupled receptor comprising hCHN4(V236K).
54. A non-endogenous version of a human G protein-coupled receptor encoded by the
cDNA of claim 53.
55. A Plasmid comprising a Vector and the cDNA of claim 53.
56. A Host Cell comprising the Plasmid of claim 55.
- 20 57. A cDNA encoding a non-endogenous, constitutively activated version of a human
G protein-coupled receptor comprising hMC4(A244K).
58. A non-endogenous version of a human G protein-coupled receptor encoded by the
cDNA of claim 57.

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59. A Plasmid comprising a Vector and the cDNA of claim 57.
60. A Host Cell comprising the Plasmid of claim 60.
61. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hCHN3(S284K).
- 5 62. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 61.
63. A Plasmid comprising a Vector and the cDNA of claim 61.
64. A Host Cell comprising the Plasmid of claim 63.
65. A cDNA encoding a non-endogenous, constitutively activated version of a human
- 10 G protein-coupled receptor comprising hCHN6(L352K).
66. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 65.
67. A Plasmid comprising a Vector and the cDNA of claim 65.
68. A Host Cell comprising the Plasmid of claim 67.
- 15 69. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hCHN8(N235K).
70. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 69.
71. A Plasmid comprising a Vector and the cDNA of claim 69.
- 20 72. A Host Cell comprising the Plasmid of claim 71.
73. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hH9(F236K).
74. A non-endogenous version of a human G protein-coupled receptor encoded by the

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cDNA of claim 73.

75. A Plasmid comprising a Vector and the cDNA of claim 73.

76. A Host Cell comprising the Plasmid of claim 74.

77. A cDNA encoding a non-endogenous, constitutively activated version of a human

5 G protein-coupled AT1 receptor selected from the group consisting of:

hAT1(F239K); hAT1(N111A); hAT1(AT2K255IC3); and hAT1(A243+).

78. A non-endogenous version of a human G protein-coupled receptor encoded by a

cDNA of claim 77.

79. A Plasmid comprising a Vector and the cDNA of claim 77.

10 80. A Host Cell comprising the Plasmid of claim 79.

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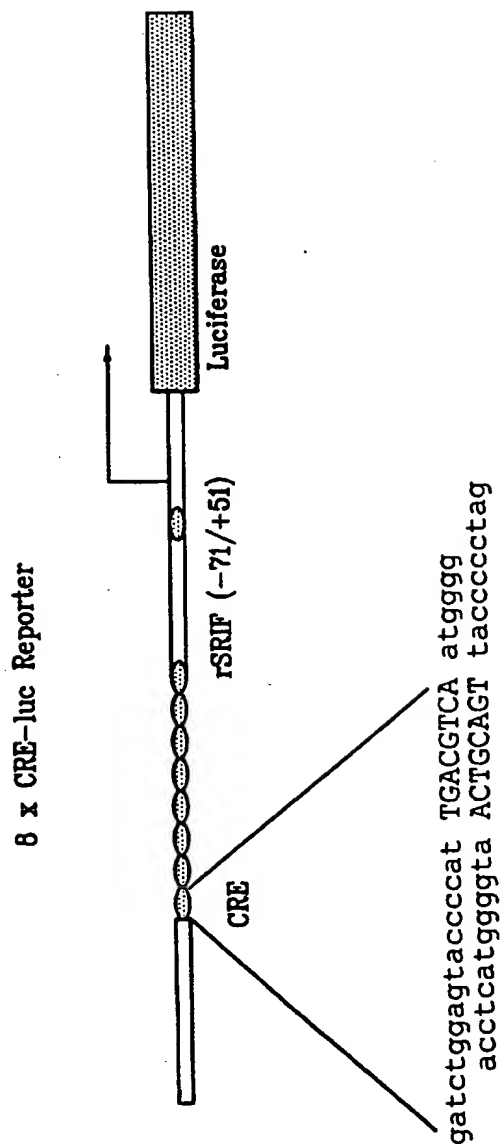


FIG. 1

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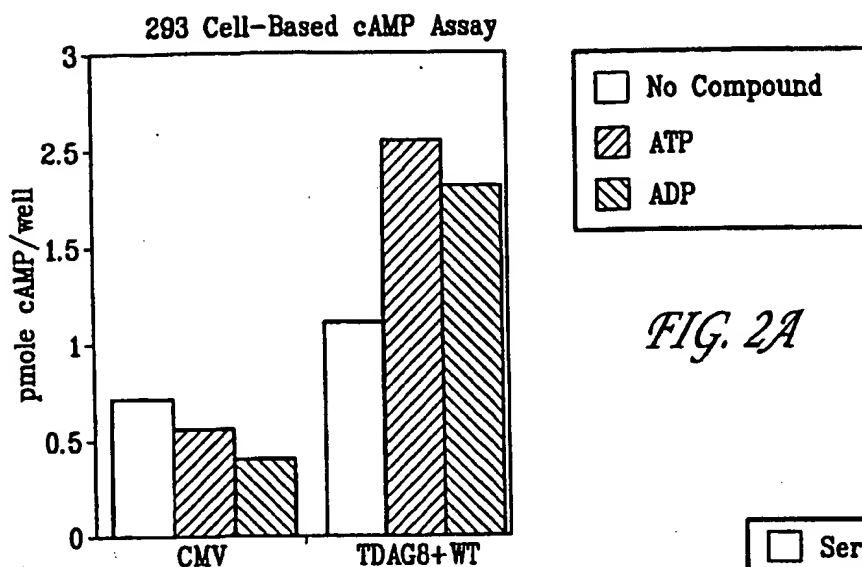


FIG. 2A

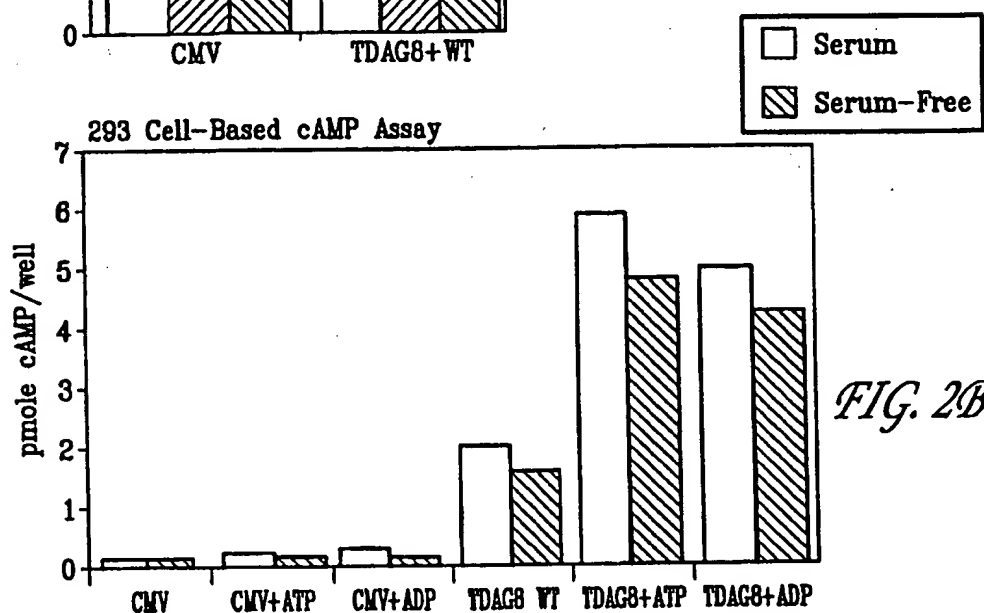


FIG. 2B

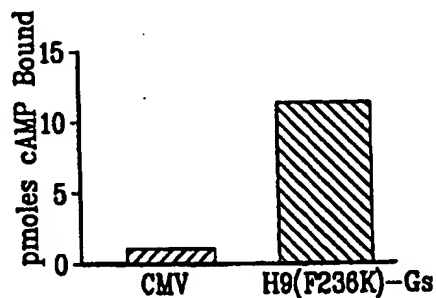


FIG. 3

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Behan, Dominic P.
Lehmann-Bruinsma, Karin
Chalmers, Derek T.
Lowitz, Kevin P.
Lin, I-Lin
10 Dang, Huong T.
Chen, Ruoping
Liaw, Chen W.
Gore, Martin J.
White, Carol
- 15 (ii) TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
Protein-Coupled Receptors
- (iii) NUMBER OF SEQUENCES: 146
- (iv) CORRESPONDENCE ADDRESS:
20 (A) ADDRESSEE: Arena Pharmaceuticals, Inc.
(B) STREET: 6166 Nancy Ridge Drive
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92121
- 25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Burgoon, Richard P.
(B) REGISTRATION NUMBER: 34,787
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (858)453-7200
(B) TELEFAX: (858)453-7210
- 40 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	ATGGTCTTCT	CGGCAGTGTT	GACTGCGTTC	CATACCGGGA	CATCCAACAC	AACATTTGTC	60
5	GTGTATGAAA	ACACCTACAT	GAATATTACA	CTCCCTCCAC	CATTCCAGCA	TCCTGACCTC	120
	AGTCCATTGC	TTAGATATAG	TTTGAAGACC	ATGGCTCCCA	CTGGTTTGAG	TTCTTGACC	180
	GTGAATAGTA	CAGCTGTGCC	CACAACACCA	GCAGCATTTA	AGAGCCTAAA	CTTGCTCTT	240
	CAGATCACCC	TTTCTGCTAT	AATGATATTC	ATTCTGTTTG	TGTCTTTTCT	TGGGAACCTG	300
	GTTGTTTGCC	TCATGGTTTA	CCAAAAGCT	GCCATGAGGT	CTGCAATTAA	CATCCTCCTT	360
10	GCCAGCCTAG	CTTTTGACAG	CATGTTGCTT	GCAGTGCTGA	ACATGCCCTT	TGCCCTGGTA	420
	ACTATCTTA	CTACCCGATG	GATTTTTGGG	AAATCTTCT	GTAGGGTATC	TGCTATGTTT	480
	TTCTGTTAT	TTGTGATAGA	AGGAGTAGCC	ATCCTGCTCA	TCATTAGCAT	AGATAGGTTC	540
	CTTATTATAG	TCCAGAGGCA	GGATAAGCTA	AACCCATATA	GAGCTAAGGT	TCTGATTGCA	600
	GTTTCTTGGG	CAACTTCCTT	TTGTGTAGCT	TTTCCTTTAG	CCGTAGGAAA	CCCCGACCTG	660
15	CAGATACCTT	CCCGAGCTCC	CCAGTGTGTG	TTGGGTACA	CAACCAATCC	AGGCTACCAG	720
	GCTTATGTGA	TTTGTATTC	TCTCATTCT	TTCTTCATAC	CCTTCCTGGT	AATACTGTAC	780
	TCATTTATGG	GCATACTCAA	CACCTTCGG	CACAATGCCT	TGAGGATCCA	TAGCTACCTT	840
	GAAGGTATAT	GCCTCAGCCA	GGCCAGCAA	CTGGGTCTCA	TGAGTCTGCA	GAGACCTTTC	900
	CAGATGAGCA	TTGACATGGG	CTTTAAACAA	CGTGCCTTCA	CCACTATTTT	GATTCTCTTT	960
20	GCTGTCTTCA	TTGTCTGCTG	GGCCCCATTC	ACCACTTACA	GCCTTGTTGGC	AACATTCAGT	1020
	AAGCACTTTT	ACTATCAGCA	CAACTTTTTT	GAGATTAGCA	CCTGGCTACT	GTGGCTCTGC	1080
	TACCTCAAGT	CTGCATTGAA	TCCGCTGATC	TACTACTGGA	GGATTAAGAA	ATTCCATGAT	1140
	GCTTGCTTGG	ACATGATGCC	TAAGTCCTTC	AAGTTTTTGC	CGCAGCTCCC	TGGTCACACA	1200
	AAGCGACGGA	TACGTCTTAG	TGCTGTCTAT	GTGTGTGGGG	AACATCGGAC	GGTGGTGTGA	1260

25 (3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Val	Phe	Ser	Ala	Val	Leu	Thr	Ala	Phe	His	Thr	Gly	Thr	Ser	Asn	
	1				5					10					15		
5	Thr	Thr	Phe	Val	Val	Tyr	Glu	Asn	Thr	Tyr	Met	Asn	Ile	Thr	Leu	Pro	
				20					25					30			
	Pro	Pro	Phe	Gln	His	Pro	Asp	Leu	Ser	Pro	Leu	Leu	Arg	Tyr	Ser	Phe	
				35				40					45				
10	Glu	Thr	Met	Ala	Pro	Thr	Gly	Leu	Ser	Ser	Leu	Thr	Val	Asn	Ser	Thr	
	-50						55					60					
	Ala	Val	Pro	Thr	Thr	Pro	Ala	Ala	Phe	Lys	Ser	Leu	Asn	Leu	Pro	Leu	
	65					70				75					80		
	Gln	Ile	Thr	Leu	Ser	Ala	Ile	Met	Ile	Phe	Ile	Leu	Phe	Val	Ser	Phe	
				85						90					95		
15	Leu	Gly	Asn	Leu	Val	Val	Cys	Leu	Met	Val	Tyr	Gln	Lys	Ala	Ala	Met	
				100					105						110		
	Arg	Ser	Ala	Ile	Asn	Ile	Leu	Leu	Ala	Ser	Leu	Ala	Phe	Ala	Asp	Met	
				115				120					125				
20	Leu	Leu	Ala	Val	Leu	Asn	Met	Pro	Phe	Ala	Leu	Val	Thr	Ile	Leu	Thr	
	130					135						140					
	Thr	Arg	Trp	Ile	Phe	Gly	Lys	Phe	Phe	Cys	Arg	Val	Ser	Ala	Met	Phe	
	145					150					155				160		
	Phe	Trp	Leu	Phe	Val	Ile	Glu	Gly	Val	Ala	Ile	Leu	Leu	Ile	Ile	Ser	
				165					170					175			
25	Ile	Asp	Arg	Phe	Leu	Ile	Ile	Val	Gln	Arg	Gln	Asp	Lys	Leu	Asn	Pro	
				180					185					190			
	Tyr	Arg	Ala	Lys	Val	Leu	Ile	Ala	Val	Ser	Trp	Ala	Thr	Ser	Phe	Cys	
				195				200					205				
30	Val	Ala	Phe	Pro	Leu	Ala	Val	Gly	Asn	Pro	Asp	Leu	Gln	Ile	Pro	Ser	
	210					215						220					
	Arg	Ala	Pro	Gln	Cys	Val	Phe	Gly	Tyr	Thr	Thr	Asn	Pro	Gly	Tyr	Gln	
	225				230						235				240		
	Ala	Tyr	Val	Ile	Leu	Ile	Ser	Leu	Ile	Ser	Phe	Phe	Ile	Pro	Phe	Leu	
				245					250					255			
35	Val	Ile	Leu	Tyr	Ser	Phe	Met	Gly	Ile	Leu	Asn	Thr	Leu	Arg	His	Asn	
				260					265					270			

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Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala
 275 280 285

Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile
 290 295 300

5 Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe
 305 310 315 320

Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val
 325 330 335

Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile
 10 340 345 350

Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro
 355 360 365

Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp
 370 375 380

15 Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr
 385 390 395 400

Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg
 405 410 415

Thr Val Val
 20

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTAGCCA ACAGCTCCTC AACCAACAGT TCTGTTCTCC CGTGTCTCTGA CTACCGACCT 60

30 ACCCACC GCC TGCACCTGGT GGTCTACAGC TTGGTGCTGG CTGCCGGGCT CCCCCTCAAC 120

GCGCTAGCCC TCTGGGTCTT CCTGCGCGCG CTGCGCGTGC ACTCGGTGGT GAGCGTGTAC 180

ATGTGTAACC TGGCGGCCAG CGACCTGCTC TTCACCTCT CTGCTGCCCGT TCGTCTCTCC 240

TACTACGCAC TGCACCACTG GCCCTTCCCC GACCTCCTGT GCCAGACGAC GGGCGCCATC 300

TTCCAGATGA ACATGTACGG CAGCTGCATC TTCTGTATGC TCATCAACGT GGACCGCTAC 360

- 5 -

GCCGCCATCG TGCACCCGCT GCGACTGCGC CACCTGCGGC GGCCCCGCGT GGCGCGGCTG 420
 CTCTGCCTGG GCGTGTGGGC GCTCATCCTG GTGTTTGCCG TGCCCGCCGC CCGCGTGCAC 480
 AGGCCCTCGC GTTGCCGCTA CCGGGACCTC GAGGTGCGCC TATGCTTCGA GAGCTTCAGC 540
 GACGAGCTGT GGAAAGGCAG GCTGTGCCCC CTCGTGCTGC TGGCCGAGGC GCTGGGCTTC 600
 5 CTGCTGCCCC TGGCGGCGGT GGTCTACTCG TCGGGCCGAG TCTTCTGGAC GCTGGCGCGC 660
 CCCGACGCCA CGCAGAGCCA GCGGCGGCGG AAGACCGTGC GCCTCCTGCT GGCTAACCTC 720
 GTCATCTTCC TGCTGTGCTT CGTGCCCTAC AACAGCACGC TGGCGGTCTA CGGGCTGCTG 780
 CGGAGCAAGC TGGTGGCGGC CAGCGTGCCT GCCCGCGATC GCGTGCGCGG GGTGCTGATG 840
 GTGATGGTGC TGCTGGCCGG CGCCAACTGC GTGCTGGACC CGCTGGTGTA CTACTTTAGC 900
 10 GCCGAGGGCT TCCGCAACAC CCTGCGCGGC CTGGGCACTC CGCACCGGGC CAGGACCTCG 960
 GCCACCAACG GGACGCGGGC GCGCTCGCG CAATCCGAAA GGTCCGCCGT CACCACCGAC 1020
 GCCACCAGGC CGGATGCCGC CAGTCAGGGG CTGCTCCGAC CCTCCGACTC CCACTCTCTG 1080
 TCTTCCTTCA CACAGTGTC CAGGATTCC GCCCTCTGA 1119

(5) INFORMATION FOR SEQ ID NO:4:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Ala Asn Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro
 1 5 10 15
 Asp Tyr Arg Pro Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val
 25 20 25 30
 Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu
 35 40 45
 Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu
 50 55 60
 30 Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser
 65 70 75 80
 Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr

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	85	90	95
	Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu		
	100	105	110
5	Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg		
	115	120	125
	Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly		
	130	135	140
	Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His		
	145	150	155
10	Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe		
	165	170	175
	Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val		
	180	185	190
15	Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val		
	195	200	205
	Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr		
	210	215	220
	Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu		
	225	230	235
20	Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val		
	245	250	255
	Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg		
	260	265	270
25	Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala		
	275	280	285
	Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe		
	290	295	300
	Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser		
	305	310	315
30	Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala		
	325	330	335
	Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu		
	340	345	350
35	Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln		
	355	360	365
	Asp Ser Ala Leu		
	370		

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(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	ATGGCCAACT CCACAGGGCT GAACGCCTCA GAAGTCGCAG GCTCGTTGGG GTTGATCCTG	60
10	GCAGCTGTCTG TGGAGGTGGG GGCAGTCTG GCAACGGCG CGCTGCTGGT CGTGGTGTCTG	120
	CGCAGCCCGG GACTGCGCGA CGCGCTCTAC CTGGCGCACC TGTGCGTCGT GGACCTGTCTG	180
	GCGGCCGCCT CCATCATGCC GCTGGGCCTG CTGGCCGCAC CGCCGCCCGG GCTGGGCCCGC	240
	GTGCGCCTGG GCGCCGCGCC ATGCCGCGCC GCTCGCTTCC TCTCCGCCGC TCTGCTGCCG	300
	GCCTGCACGC TCGGGGTGGC CGCACTTGGC CTGGCACGCT ACCGCCTCAT CGTGCACCCG	360
15	CTGCGGCCAG GCTCGCGGCC GCCGCCTGTG CTCGTGCTCA CCGCCGTGTG GGCCGCGGCG	420
	GGACTGCTGG GCGCGCTCTC CCTGTCTGGC CCGCCGCCCG CACCGCCCCC TGCTCCTGCT	480
	CGCTGCTCGG TCCTGGCTGG GGGCCTCGGG CCCTTCCGGC CGCTCTGGGC CCTGCTGGCC	540
	TTGCGCTGC CCGCCCTCCT GCTGCTCGGC GCCTACGGCG GCATCTTCGT GGTGGCGCGT	600
	CGCGCTGCCC TGAGGCCCCC ACGGCCGGCG CGCGGGTCCC GACTCCGCTC GGACTCTCTG	660
20	GATAGCCGCC TTTCATCTT GCCGCCGCTC CGGCCTCGCC TGCCCGGGGG CAAGGCGGCC	720
	CTGGCCCCAG CGCTGGCCGT GGGCCAATTT GCAGCCTGCT GGCTGCCTTA TGGCTGCGCG	780
	TGCCTGGCGC CCGCAGCGCG GGCCGCGGAA GCCGAAGCGG CTGTCACTG GGTGCGCTAC	840
	TCGGCCTTCG CGGCTCACCC CTTCCTGTAC GGGCTGCTGC AGCGCCCCGT GCGCTTGGCA	900
	CTGGGCCGCC TCTCTCGCCG TGCACTGCCT GGACCTGTGC GGGCCTGCAC TCCGCAAGCC	960
25	TGGCAGCCGC GGGCACTCTT GCAATGCCTC CAGAGACCCC CAGAGGGCCC TGCCGTAGGC	1020
	CCTTCTGAGG CTCCAGAACA GACCCCGAG TTGGCAGGAG GCGGAGCCC CGCATAACCAG	1080
	GGGCCACCTG AGAGTTCTCT CTCCTGA	1107

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	Met	Ala	Asn	Ser	Thr	Gly	Leu	Asn	Ala	Ser	Glu	Val	Ala	Gly	Ser	Leu	
	1				5					10					15		
	Gly	Leu	Ile	Leu	Ala	Ala	Val	Val	Glu	Val	Gly	Ala	Leu	Leu	Gly	Asn	
			20						25					30			
10	Gly	Ala	Leu	Leu	Val	Val	Val	Leu	Arg	Thr	Pro	Gly	Leu	Arg	Asp	Ala	
		35						40					45				
	Leu	Tyr	Leu	Ala	His	Leu	Cys	Val	Val	Asp	Leu	Leu	Ala	Ala	Ala	Ser	
		50					55					60					
15	Ile	Met	Pro	Leu	Gly	Leu	Leu	Ala	Ala	Pro	Pro	Pro	Gly	Leu	Gly	Arg	
	65					70					75				80		
	Val	Arg	Leu	Gly	Pro	Ala	Pro	Cys	Arg	Ala	Ala	Arg	Phe	Leu	Ser	Ala	
					85					90					95		
	Ala	Leu	Leu	Pro	Ala	Cys	Thr	Leu	Gly	Val	Ala	Ala	Leu	Gly	Leu	Ala	
				100					105					110			
20	Arg	Tyr	Arg	Leu	Ile	Val	His	Pro	Leu	Arg	Pro	Gly	Ser	Arg	Pro	Pro	
			115						120				125				
	Pro	Val	Leu	Val	Leu	Thr	Ala	Val	Trp	Ala	Ala	Ala	Gly	Leu	Leu	Gly	
		130					135						140				
25	Ala	Leu	Ser	Leu	Leu	Gly	Pro	Pro	Pro	Ala	Pro	Pro	Pro	Ala	Pro	Ala	
	145					150					155				160		
	Arg	Cys	Ser	Val	Leu	Ala	Gly	Gly	Leu	Gly	Pro	Phe	Arg	Pro	Leu	Trp	
				165						170					175		
	Ala	Leu	Leu	Ala	Phe	Ala	Leu	Pro	Ala	Leu	Leu	Leu	Leu	Gly	Ala	Tyr	
				180					185					190			
30	Gly	Gly	Ile	Phe	Val	Val	Ala	Arg	Arg	Ala	Ala	Leu	Arg	Pro	Pro	Arg	
			195					200					205				
	Pro	Ala	Arg	Gly	Ser	Arg	Leu	Arg	Ser	Asp	Ser	Leu	Asp	Ser	Arg	Leu	
		210						215					220				
35	Ser	Ile	Leu	Pro	Pro	Leu	Arg	Pro	Arg	Leu	Pro	Gly	Gly	Lys	Ala	Ala	
	225					230					235				240		
	Leu	Ala	Pro	Ala	Leu	Ala	Val	Gly	Gln	Phe	Ala	Ala	Cys	Trp	Leu	Pro	

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	245	250	255
	Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu		
	260	265	270
5	Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe		
	275	280	285
	Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu		
	290	295	300
	Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala		
	305	310	315
10	Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly		
	325	330	335
	Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala		
	340	345	350
15	Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser Ser Leu Ser		
	355	360	365

(8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1008 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	ATGGAATCAT CTTTCTCATT TGGAGTGATC CTGCTGTCC TGGCCTCCCT CATCATTGCT	60
25	ACTAACACAC TAGTGGCTGT GGCTGTGCTG CTGTTGATCC ACAAGAATGA TGGTGTCACT	120
	CTCTGCTTCA CCTTGAATCT GGCTGTGGCT GACACCTTGA TTGGTGTGGC CATCTCTGGC	180
	CTACTCACAG ACCAGCTCTC CAGCCCTTCT CGGCCCACAC AGAAGACCCT GTGCAGCCTG	240
	CGGATGGCAT TTGTCACCTC CTCCGAGCT GCCTCTGTCC TCACGGTCAT GCTGATCACC	300
	TTTGACAGGT ACCTTGCCAT CAAGCAGCCC TTCCGCTACT TGAAGATCAT GAGTGGGTTC	360
30	GTGGCCGGGG CCTGCATTGC CGGGCTGTGG TTAGTGTCTT ACCTCATTGG CTTCTCTCCA	420
	CTCGGAATCC CCATGTTCCA GCAGACTGCC TACAAAGGGC AGTGCAGCTT CTTTGCTGTA	480
	TTTCAACCTC ACTTCGTGCT GACCCCTCTC TGCCTTGGCT TCTTCCAGC CATGCTCCTC	540
	TTTGTCTTCT TCTACTGCGA CATGCTCAAG ATTGCCTCCA TGCACAGCCA GCAGATTCCA	600

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AAGATGGAAC ATGCAGGAGC CATGGCTGGA GGTATCGAT CCCCACGGAC TCCCAGCGAC 660
 TTCAAAGCTC TCCGTACTGT GTCTGTTCTC ATTGGGAGCT TTGCTCTATC CTGGACCCCC 720
 TTCCTTATCA CTGGCATTGT GCAGGTGGCC TGCCAGGAGT GTCACCTCTA CCTAGTGCTG 780
 GAACGGTACC TGTGGCTGCT CGGCGTGGGC AACTCCCTGC TCAACCCACT CATCTATGCC 840
 5 TATTGGCAGA AGGAGGTGCG ACTGCAGCTC TACCACATGG CCCTAGGAGT GAAGAAGGTG 900
 CTCACCTCAT TCCTCCTCTT TCTCTCGGCC AGGAATTGTG GCCCAGAGAG GCCCAGGGAA 960
 AGTTCCTGTC ACATCGTCAC TATCTCCAGC TCAGAGTTTG ATGGCTAA 1008

(9) INFORMATION FOR SEQ ID NO:8:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
 1 5 10 15
 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
 20 25 30
 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
 35 40 45
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
 50 55 60
 25 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
 65 70 75 80
 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ser Val Leu Thr Val
 85 90 95
 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
 100 105 110
 30 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
 115 120 125
 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
 130 135 140
 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val

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	145		150		155		160
	Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro						
		165		170			175
5	Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala						
		180		185			190
	Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met						
		195		200			205
	Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu						
		210		215			220
10	Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro						
		225		230			240
	Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu						
		245		250			255
15	Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser						
		260		265			270
	Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu						
		275		280			285
	Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe						
		290		295			300
20	Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu						
		305		310			320
	Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly						
		325		330			335

(10) INFORMATION FOR SEQ ID NO:9:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGACACTA CCATGGAAGC TGACCTGGGT GCCACTGGCC ACAGGCCCCG CACAGAGCTT	60
GATGATGAGG ACTCCTACCC CCAAGGTGGC TGGGACACGG TCTTCCTGGT GGCCCTGCTG	120
CTCCTTGGGC TGCCAGCCAA TGGGTTGATG GCGTGGCTGG CCGGCTCCCA GGCCCGGCAT	180
35 GGAGCTGGCA CGCGTCTGGC GCTGCTCCTG CTCAGCCTGG CCCTCTCTGA CTTCTTGTTT	240

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CTGGCAGCAG CGGCCTTCCA GATCCTAGAG ATCCGGCATG GGGGACACTG GCCGCTGGGG 300
 ACAGCTGCCT GCCGCTTCTA CTACTTCCTA TGGGGCGTGT CCTACTCCTC CGGCCTCTTC 360
 CTGCTGGCCG CCCTCAGCCT CGACCGCTGC CTGCTGGCGC TGTGCCCACA CTGGTACCCT 420
 GGGCACC GCCCAGTCCGCT GCGCCCTCTGG GTCTGCGCCG GTGTCTGGGT GCTGGCCACA 480
 5 CTCTTCAGCG TGCCCTGGCT GGTCTTCCCC GAGGCTGCCG TCTGGTGGTA CGACCTGGTC 540
 ATCTGCCTGG ACTTCTGGGA CAGCGAGGAG CTGTCGCTGA GGATGCTGGA GGTCTGGGG 600
 GGCTTCCTGC CTTTCCTCCT GCTGCTCGTC TGCCACGTGC TCACCCAGGC CACAGCCTGT 660
 CGCACCTGCC ACCGCCAACA GCAGCCCGCA GCCTGCCGGG GCTTCGCCCCG TGTGGCCAGG 720
 ACCATTCTGT CAGCCTATGT GGTCTGAGG CTGCCCTACC AGCTGGCCCA GCTGCTCTAC 780
 10 CTGGCCTTCC TGTGGGACGT CTACTCTGGC TACCTGCTCT GGGAGGCCCT GGTCTACTCC 840
 GACTACCTGA TCCTACTCAA CAGCTGCCTC AGCCCCTTCC TCTGCCTCAT GGCCAGTGCC 900
 GACCTCCGGA CCCTGCTGCG CTCCGTGCTC TCGTCCTTCG CGGCAGCTCT CTGCGAGGAG 960
 CGGCCGGGCA GCTTCACGCC CACTGAGCCA CAGACCCAGC TAGATTCTGA GGGTCCAAC 1020
 CTGCCAGAGC CGATGGCAGA GGCCCACTCA CAGATGGATC CTGTGGCCCA GCCTCAGGTG 1080
 15 AACCCACAC TCCAGCCACG ATCGGATCCC ACAGCTCAGC CACAGCTGAA CCCTACGGCC 1140
 CAGCCACAGT CGGATCCCAC AGCCCAAGCA CAGCTGAACC TCATGGCCCA GCCACAGTCA 1200
 GATTCTGTGG CCCAGCCACA GGCAGACACT AACGTCCAGA CCCCTGCACC TGCTGCCAGT 1260
 TCTGTGCCCA GTCCCTGTGA TGAAGCTTCC CCAACCCCAT CCTCGCATCC TACCCAGGG 1320
 GCCCTTGAGG ACCCAGCCAC ACCTCCTGCC TCTGAAGGAG AAAGCCCCAG CAGCACCCG 1380
 20 CCAGAGGCGG CCCCAGGCGC AGGCCCCACG TGA 1413

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30 Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro
 1 5 10 15

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	Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp	20	25	30
	Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly	35	40	45
5	Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr	50	55	60
	Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe	65	70	75
				80
10	Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His	85	90	95
	Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly	100	105	110
	Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp	115	120	125
15	Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro	130	135	140
	Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr	145	150	155
				160
20	Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp	165	170	175
	Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser	180	185	190
	Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu	195	200	205
25	Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln	210	215	220
	Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile	225	230	235
				240
30	Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu	245	250	255
	Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp	260	265	270
	Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu	275	280	285
35	Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu	290	295	300
	Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro			

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	305		310		315		320
	Gly Ser Phe Thr	Pro Thr Glu Pro Gln Thr	Gln Leu Asp Ser	Glu Gly			
		325		330		335	
5	Pro Thr Leu Pro	Glu Pro Met Ala Glu Ala Gln Ser	Gln Met Asp Pro				
		340		345		350	
	Val Ala Gln Pro	Gln Val Asn Pro Thr Leu Gln Pro	Arg Ser Asp Pro				
		355		360		365	
	Thr Ala Gln Pro	Gln Leu Asn Pro Thr Ala Gln Pro	Gln Ser Asp Pro				
		370		375		380	
10	Thr Ala Gln Pro	Gln Leu Asn Leu Met Ala Gln Pro	Gln Ser Asp Ser				
		385		390		395	400
	Val Ala Gln Pro	Gln Ala Asp Thr Asn Val Gln Thr	Pro Ala Pro Ala				
		405		410		415	
15	Ala Ser Ser Val	Pro Ser Pro Cys Asp Glu Ala Ser	Pro Thr Pro Ser				
		420		425		430	
	Ser His Pro Thr	Pro Gly Ala Leu Glu Asp Pro Ala Thr	Pro Pro Ala				
		435		440		445	
	Ser Glu Gly Glu	Ser Pro Ser Ser Thr Pro Pro Glu Ala	Ala Pro Gly				
		450		455		460	
20	Ala Gly Pro Thr						
	465						

(12) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30	ATGTCAGGGA TGGAAAACT TCAGAATGCT TCCTGGATCT ACCAGCAGAA ACTAGAAGAT	60
	CCATTCCAGA AACACCTGAA CAGCACCGAG GAGTATCTGG CCTTCCTCTG CGGACCTCGG	120
	CGCAGCCACT TCTTCCTCCC CGTGTCTGTG GTGTATGTGC CAATTTTGTG GGTGGGGGTC	180
	ATTGGCAATG TCCTGGTGTG CCTGGTGATT CTGCAGCACC AGGCTATGAA GACGCCCACC	240
	AACTACTACC TCTTCAGCCT GCGGTCTCT GACCTCCTGG TCCTGCTCCT TGAATGCCC	300

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CTGGAGGTCT ATGAGATGTG GCGCAACTAC CCTTTCTTGT TCGGGCCCGT GGGCTGCTAC 360
 TTCAAGACGG CCCTCTTTGA GACCGTGTGC TTCGCCTCCA TCCTCAGCAT CACCACCGTC 420
 AGCGTGGAGC GCTACGTGGC CATCCTACAC CCGTTCCGCG CCAAAGTGA GAGCACCCGG 480
 CGCCGGGGCCC TCAGGATCCT CGGCATCGTC TGGGGCTTCT CCGTGCTCTT CTCCCTGCCC 540
 5 AACACCAGCA TCCATGGCAT CAAGTTCCAC TACTTCCCCA ATGGGTCCCT GGTCCCAGGT 600
 TCGGCCACCT GTACGGTCAT CAAGCCCATG TGGATCTACA ATTTTCATCAT CCAGGTCACC 660
 TCCTTCCTAT TCTACCTCCT CCCCATGACT GTCATCAGTG TCCTCTACTA CCTCATGGCA 720
 CTCAGACTAA AGAAAGACAA ATCTCTTGAG GCAGATGAAG GGAATGCAAA TATTCAAAGA 780
 CCCTGCAGAA AATCAGTCAA CAAGATGCTG TTTGTCTTGG TCTTAGTGTT TGCTATCTGT 840
 10 TGGGCCCCCGT TCCACATTGA CCGACTCTTC TTCAGCTTTG TGGAGGAGTG GAGTGAATCC 900
 CTGGCTGCTG TGTTCAACCT CGTCCATGTG GTGTCAGGTG TCTTCTTCTA CCTGAGCTCA 960
 GCTGTCAACC CCATTATCTA TAACCTACTG TCTCGCCGCT TCCAGGCAGC ATTCCAGAAT 1020
 GTGATCTCTT CTTTCCACAA ACAGTGGCAC TCCCAGCATG ACCCAGAGTT GCCACCTGCC 1080
 CAGCGGAACA TCTTCCTGAC AGAATGCCAC TTTGTGGAGC TGACCGAAGA TATAGGTCCC 1140
 15 CAATTCCCAT GTCAGTCATC CATGCACAAC TCTCACCTCC CAACAGCCCT CTCTAGTGAA 1200
 CAGATGTCAA GAACAACTA TCAAAGCTTC CACTTTAACA AAACCTGA 1248

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 415 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25

Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln
 1 5 10 15

Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
 20 25 30

30

Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
 35 40 45

Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val

50				55				60							
Leu 65	Val	Cys	Leu	Val	Ile 70	Leu	Gln	His	Gln	Ala 75	Met	Lys	Thr	Pro	Thr 80
Asn	Tyr	Tyr	Leu	Phe 85	Ser	Leu	Ala	Val	Ser 90	Asp	Leu	Leu	Val	Leu 95	Leu
Leu	Gly	Met	Pro	Leu	Glu	Val	Tyr	Glu 105	Met	Trp	Arg	Asn	Tyr	Pro	Phe
Leu	Phe	Gly 115	Pro	Val	Gly	Cys	Tyr 120	Phe	Lys	Thr	Ala	Leu 125	Phe	Glu	Thr
Val	Cys 130	Phe	Ala	Ser	Ile	Leu 135	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg
Tyr 145	Val	Ala	Ile	Leu	His 150	Pro	Phe	Arg	Ala	Lys 155	Leu	Gln	Ser	Thr	Arg 160
Arg	Arg	Ala	Leu	Arg 165	Ile	Leu	Gly	Ile	Val 170	Trp	Gly	Phe	Ser	Val	Leu 175
Phe	Ser	Leu	Pro	Asn 180	Thr	Ser	Ile	His 185	Gly	Ile	Lys	Phe	His 190	Tyr	Phe
Pro	Asn	Gly 195	Ser	Leu	Val	Pro	Gly 200	Ser	Ala	Thr	Cys	Thr 205	Val	Ile	Lys
Pro	Met 210	Trp	Ile	Tyr	Asn	Phe 215	Ile	Ile	Gln	Val	Thr 220	Ser	Phe	Leu	Phe
Tyr 225	Leu	Leu	Pro	Met	Thr 230	Val	Ile	Ser	Val	Leu 235	Tyr	Tyr	Leu	Met	Ala 240
Leu	Arg	Leu	Lys 245	Lys	Asp	Lys	Ser	Leu	Glu 250	Ala	Asp	Glu	Gly	Asn 255	Ala
Asn	Ile	Gln	Arg 260	Pro	Cys	Arg	Lys 265	Ser	Val	Asn	Lys	Met	Leu	Phe 270	Val
Leu	Val	Leu	Val	Phe	Ala	Ile	Cys 280	Trp	Ala	Pro	Phe	His 285	Ile	Asp	Arg
Leu	Phe 290	Phe	Ser	Phe	Val	Glu 295	Glu	Trp	Ser	Glu	Ser 300	Leu	Ala	Ala	Val
Phe 305	Asn	Leu	Val	His 310	Val	Val	Ser	Gly	Val	Phe 315	Phe	Tyr	Leu	Ser	Ser 320
Ala	Val	Asn	Pro	Ile 325	Ile	Tyr	Asn	Leu	Leu 330	Ser	Arg	Arg	Phe	Gln 335	Ala
Ala	Phe	Gln	Asn 340	Val	Ile	Ser	Ser	Phe 345	His	Lys	Gln	Trp	His 350	Ser	Gln

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His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
355 360 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
370 375 380

5 Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
405 410 415

(14) INFORMATION FOR SEQ ID NO:13:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCCAGATA CTAATAGCAC AATCAATTTA TCACTAAGCA CTCGTGTTAC TTTAGCATTT 60
 TTTATGTCCT TAGTAGCTTT TGCTATAATG CTAGGAAATG CTTTGGTCAT TTTAGCTTTT 120
 GTGGTGGACA AAAACCTTAG ACATCGAAGT AGTTATTTT TTCTTAACCT GGCCATCTCT 180
 20 GACTTCTTTG TGGGTGTGAT CTCCATTCCT TTGTACATCC CTCACACGCT GTTCGAATGG 240
 GATTTTGGAA AGGAAATCTG TGTATTTTGG CTCACTACTG ACTATCTGTT ATGTACAGCA 300
 TCTGTATATA ACATTGTCCT CATCAGCTAT GATCGATACC TGTCACTCTC AAATGCTGTG 360
 TCTTATAGAA CTCAACATAC TGGGGTCTTG AAGATTGTTA CTCTGATGGT GGCCGTTTGG 420
 GTGCTGGCCT TCTTAGTGAA TGGGCCAATG ATTCTAGTTT CAGAGTCTTG GAAGGATGAA 480
 25 GGTAGTGAAT GTGAACCTGG ATTTTTCG GAATGGTACA TCCTTGCCAT CACATCATTC 540
 TTGGAATTCG TGATCCCACT CATCTTAGTC GCTTATTTC ACATGAATAT TTATTGGAGC 600
 CTGTGGAAGC GTGATCATCT CAGTAGGTGC CAAAGCCATC CTGGACTGAC TGCTGTCTCT 660
 TCCAACATCT GTGGACACTC ATTCAGAGGT AGACTATCTT CAAGGAGATC TCTTTCTGCA 720
 TCGACAGAAG TTCCTGCATC CTTTCATTCA GAGAGACAGA GGAGAAAGAG TAGTCTCATG 780
 30 TTTTCTCAA GAACCAAGAT GAATAGCAAT ACAATTGCTT CAAAATGGG TTCCTTCTCC 840
 CAATCAGATT CTGTAGCTCT TCACCAAAGG GAACATGTTG AACTGCTTAG AGCCAGGAGA 900

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TTAGCCAAGT CACTGGCCAT TCTCTTAGGG GTTTTGTCTG TTTGCTGGGC TCCATATTCT 960
 CTGTTACAAA TTGTCCTTTC ATTTTATTC TCAGCAACAG GTCCTAAATC AGTTTGGTAT 1020
 AGAATTGCAT TTTGGCTTCA GTGGTTCAAT TCCTTTGTCA ATCCTCTTTT GTATCCATTG 1080
 TGTCAACAAGC GCTTTCAAAA GGCTTTCTTG AAAATATTTT GTATAAAAAA GCAACCTCTA 1140
 5 CCATCACAAC ACAGTCGGTC AGTATCTTCT TAA 1173

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
 (B) TYPE: amino acid
 10 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val
 15 1 5 10 15
 Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly
 20 20 25 30
 Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His
 35 40 45
 20 Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val
 50 55 60
 Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp
 65 70 75 80
 25 Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu
 85 90 95
 Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg
 100 105 110
 Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly
 115 120 125
 30 Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe
 130 135 140
 Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu
 145 150 155 160
 35 Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala
 165 170 175

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Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr
180 185 190

Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser
195 200 205

5 Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys
210 215 220

Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala
225 230 235 240

10 Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys
245 250 255

Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile
260 265 270

Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His
275 280 285

15 Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser
290 295 300

Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser
305 310 315 320

20 Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys
325 330 335

Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe
340 345 350

Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala
355 360 365

25 Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His
370 375 380

Ser Arg Ser Val Ser Ser
385 390

(16) INFORMATION FOR SEQ ID NO:15:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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GGAAAGCTTA ACGATCCCCA GGAGCAACAT

30

(17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) ANTI-SENSE: YES

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGGGATCCT ACGAGAGCAT TTTTCACACA G

31

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGCGAACG CGAGCGAGCC GGGTGGCAGC GCGGCGGCG AGGCGGCCGC CCTGGGCCTC 60
AAGCTGGCCA CGCTCAGCCT GCTGCTGTGC GTGAGCCTAG CGGGCAACGT GCTGTTGCGG 120
CTGCTGATCG TGCGGGAGCG CAGCCTGCAC CGCGCCCCGT ACTACCTGCT GCTCGACCTG 180
TGCCTGGCCG ACGGGCTGCG CGCGCTCGCC TGCCTCCCG CCGTCATGCT GCGGCGCGCG 240
25 CGTGCGGCGG CCGCGGCGGG GCGCCGCGG GCGCGCTGG GCTGCAAGCT GCTCGCCTTC 300
CTGGCCGCGC TCTTCTGCTT CCACGCCGCC TTCCTGCTGC TGGGCGTGGG CGTCACCCGC 360
TACCTGGCCA TCGCGCACCA CCGCTTCTAT GCAGAGCGCC TGGCCGGCTG GCCGTGCGCC 420
GCCATGCTGG TGTGCGCCGC CTGGGCGCTG GCGCTGGCCG CGGCCTTCCC GCCAGTGCTG 480
GACGGCGGTG GCGACGACGA GGACGCGCCG TCGGCCCTGG AGCAGCGGCC CGACGGCGCC 540
30 CCCGGCGCGC TGGGCTTCCT GCTGCTGCTG GCCGTGGTGG TGGGCGCCAC GCACCTCGTC 600
TACCTCCGCC TGCTCTTCTT CATCCACGAC CGCCGCAAGA TCGGCCCCGC GCGCTGGTG 660

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CCCCCGGTCA GCCACGACTG GACCTTCCAC GGCCCGGGCG CCACCGGCCA GGCGGCCGCC      720
AACTGGACGG CGGGCTTCGG CCGCGGGCCC ACGCGGCCCG CGCTTGTTGG CATCCGGCCC      780
GCAGGGCCCG GCCGCGGCGC GCGCCGCCTC CTCGTGCTGG AAGAATTCAA GACGGAGAAG      840
AGGCTGTGCA AGATGTTCTA CGCCGTCACG CTGCTCTTCC TGCTCCTCTG GGGGCCCTAC      900
5  GTCGTGGCCA GCTACCTGCG GGTCTGGTG CGGCCCGGCG CCGTCCCCCA GGCCTACCTG      960
ACGGCCTCCG TGTGGCTGAC CTTGCGCAG GCCGGCATCA ACCCGTCGT GTGCTTCCTC      1020
TTCAACAGGG AGCTGAGGGA CTGCTTCAGG GCCCAGTTCC CCTGCTGCCA GAGCCCCCGG      1080
ACCACCCAGG CGACCCATCC CTGCGACCTG AAAGGCATTG GTTTATGA      1128

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(19) INFORMATION FOR SEQ ID NO:18:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala
1           5           10           15
Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser
20          20          25          30
Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
35          40          45
Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
50          55          60
25 Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
65          70          75          80
Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
85          90          95
Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
30          100         105         110
Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg
115         120         125
Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val
130         135         140

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	Cys	Ala	Ala	Trp	Ala	Leu	Ala	Leu	Ala	Ala	Ala	Phe	Pro	Pro	Val	Leu	
	145					150				155					160		
	Asp	Gly	Gly	Gly	Asp	Asp	Glu	Asp	Ala	Pro	Cys	Ala	Leu	Glu	Gln	Arg	
					165				170						175		
5	Pro	Asp	Gly	Ala	Pro	Gly	Ala	Leu	Gly	Phe	Leu	Leu	Leu	Leu	Ala	Val	
				180					185						190		
	Val	Val	Gly	Ala	Thr	His	Leu	Val	Tyr	Leu	Arg	Leu	Leu	Phe	Phe	Ile	
			195					200						205			
10	His	Asp	Arg	Arg	Lys	Met	Arg	Pro	Ala	Arg	Leu	Val	Pro	Ala	Val	Ser	
	210					215						220					
	His	Asp	Trp	Thr	Phe	His	Gly	Pro	Gly	Ala	Thr	Gly	Gln	Ala	Ala	Ala	
	225					230					235				240		
	Asn	Trp	Thr	Ala	Gly	Phe	Gly	Arg	Gly	Pro	Thr	Pro	Pro	Ala	Leu	Val	
				245					250						255		
15	Gly	Ile	Arg	Pro	Ala	Gly	Pro	Gly	Arg	Gly	Ala	Arg	Arg	Leu	Leu	Val	
			260					265						270			
	Leu	Glu	Glu	Phe	Lys	Thr	Glu	Lys	Arg	Leu	Cys	Lys	Met	Phe	Tyr	Ala	
			275					280					285				
20	Val	Thr	Leu	Leu	Phe	Leu	Leu	Leu	Trp	Gly	Pro	Tyr	Val	Val	Ala	Ser	
	290						295					300					
	Tyr	Leu	Arg	Val	Leu	Val	Arg	Pro	Gly	Ala	Val	Pro	Gln	Ala	Tyr	Leu	
	305				310						315				320		
	Thr	Ala	Ser	Val	Trp	Leu	Thr	Phe	Ala	Gln	Ala	Gly	Ile	Asn	Pro	Val	
				325					330					335			
25	Val	Cys	Phe	Leu	Phe	Asn	Arg	Glu	Leu	Arg	Asp	Cys	Phe	Arg	Ala	Gln	
			340						345					350			
	Phe	Pro	Cys	Cys	Gln	Ser	Pro	Arg	Thr	Thr	Gln	Ala	Thr	His	Pro	Cys	
			355					360					365				
30	Asp	Leu	Lys	Gly	Ile	Gly	Leu										
	370					375											

(20) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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ATGAACACCA CAGTGATGCA AGGCTTCAAC AGATCTGAGC GGTGCCCCAG AGACACTCGG    60
ATAGTACAGC TGGTATTCCC AGCCCTCTAC ACAGTGGTTT TCTTGACCGG CATCCTGCTG    120
AATACTTTGG CTCTGTGGGT GTTTGTTTAC ATCCCCAGCT CCTCCACCTT CATCATCTAC    180
5  CTCAAAAACA CTTTGGTGGC CGACTTGATA ATGACACTCA TGCTTCCTTT CAAAATCCTC    240
TCTGACTCAC ACCTGGCACC CTGGCAGCTC AGAGCTTTTG TGTGTCGTTT TTCTTCGGTG    300
ATATTTTATG AGACCATGTA TGTGGGCATC GTGCTGTTAG GGCTCATAGC CTTTGACAGA    360
TTCCTCAAGA TCATCAGACC TTTGAGAAAT ATTTTCTAA AAAAACCTGT TTTTGCAAAA    420
ACGGTCTCAA TCTTCATCTG GTTCTTTTGG TTCTTCATCT CCCTGCCAAA TACGATCTTG    480
10 AGCAACAAGG AAGCAACACC ATCGTCTGTG AAAAAGTGTG CTTCTTAAA GGGGCCTCTG    540
GGGCTGAAAT GGCATCAAAT GGTAAATAAC ATATGCCAGT TTATTTTCTG GACTGTTTTT    600
ATCCTAATGC TTGTGTTTTA TGTGGTTATT GCAAAAAAAG TATATGATTC TTATAGAAAG    660
TCCAAAAGTA AGGACAGAAA AAACAACAAA AAGCTGGAAG GCAAAGTATT TGTGTGTCGTG    720
GCTGTCTTCT TTGTGTGTTT TGCTCCATT CATTTTGCCA GAGTTCCATA TACTCACAGT    780
15 CAAACCAACA ATAAGACTGA CTGTAGACTG CAAAATCAAC TGTTTATTGC TAAAGAAACA    840
ACTCTCTTTT TGGCAGCAAC TAACATTTGT ATGGATCCCT TAATATACAT ATTCTTATGT    900
AAAAAATTCA CAGAAAAGCT ACCATGTATG CAAGGGAGAA AGACCACAGC ATCAAGCCAA    960
GAAAATCATA GCAGTCAGAC AGACAACATA ACCTTAGGCT GA                          1002

```

(21) INFORMATION FOR SEQ ID NO:20:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- 25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro
1           5           10           15

Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
30          20          25          30

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Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
 35 40 45
 Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
 50 55 60
 5 Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
 65 70 75 80
 Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
 85 90 95
 10 Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
 100 105 110
 Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
 115 120 125
 Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
 130 135 140
 15 Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu
 145 150 155 160
 Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
 165 170 175
 20 Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
 180 185 190
 Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
 195 200 205
 Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
 210 215 220
 25 Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
 225 230 235 240
 Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
 245 250 255
 30 Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
 260 265 270
 Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
 275 280 285
 Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
 290 295 300
 35 Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
 305 310 315 320
 Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly

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325

330

(22) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

10 ATGGCCAACA CTACCGGAGA GCCTGAGGAG GTGAGCGGCG CTCTGTCCCC ACCGTCCGCA 60
TCAGCTTATG TGAAGCTGGT ACTGCTGGGA CTGATTATGT GCGTGAGCCT GGCGGGTAAC 120
GCCATCTTGT CCCTGCTGGT GCTCAAGGAG CGTGCCCTGC ACAAGGCTCC TTACTACTTC 180
CTGCTGGACC TGTGCCTGGC CGATGGCATA CGCTCTGCCG TCTGCTTCCC CTTGTGCTG 240
GCTTCTGTGC GCCACGGCTC TTCATGGACC TTCAGTGAC TCAGCTGCAA GATTGTGGCC 300
15 TTTATGGCCG TGCTCTTTTG CTTCCATGCG GCCTTCATGC TGTTCGTCAT CAGCGTCACC 360
CGCTACATGG CCATCGCCCA CCACGCTTC TACGCCAAGC GCATGACACT CTGGACATGC 420
GCGGCTGTCA TCTGCATGGC CTGGACCCTG TCTGTGGCCA TGGCCTTCCC ACCTGTCTTT 480
GACGTGGGCA CCTACAAGTT TATTCGGGAG GAGGACCAGT GCATCTTTGA GCATCGCTAC 540
TTCAAGGCCA ATGACACGCT GGGCTTCATG CTTATGTTGG CTGTGCTCAT GGCAGCTACC 600
20 CATGCTGTCT ACGGCAAGCT GCTCCTCTTC GAGTATCGTC ACCGCAAGAT GAAGCCAGTG 660
CAGATGGTGC CAGCCATCAG CCAGAACTGG ACATTCCATG GTCCCGGGGC CACCGGCCAG 720
GCTGCTGCCA ACTGGATCGC CGGCTTTGGC CGTGGGCCCA TGCCACCAAC CCTGCTGGGT 780
ATCCGGCAGA ATGGGCATGC AGCCAGCCGG CGGCTACTGG GCATGGACGA GGTCAAGGGT 840
GAAAAGCAGC TGGGCCGCAT GTTCTACGCG ATCACACTGC TCTTTCTGCT CCTCTGGTCA 900
25 CCCTACATCG TGGCCTGCTA CTGGCGAGTG TTTGTGAAAG CCTGTGCTGT GCCCCACCGC 960
TACCTGGCCA CTGCTGTTTG GATGAGCTTC GCCCAGGCTG CCGTCAACCC AATTGTCTGC 1020
TTCCTGCTCA ACAAGGACCT CAAGAAGTGC CTGACCACTC ACGCCCCCTG CTGGGGCACA 1080
GGAGGTGCCC CGGCTCCCAG AGAACCTAC TGTGTCATGT GA 1122

(23) INFORMATION FOR SEQ ID NO:22:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

5 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	Met	Ala	Asn	Thr	Thr	Gly	Glu	Pro	Glu	Glu	Val	Ser	Gly	Ala	Leu	Ser	
	1				5					10					15		
10	Pro	Pro	Ser	Ala	Ser	Ala	Tyr	Val	Lys	Leu	Val	Leu	Leu	Gly	Leu	Ile	
				20					25					30			
	Met	Cys	Val	Ser	Leu	Ala	Gly	Asn	Ala	Ile	Leu	Ser	Leu	Leu	Val	Leu	
		35						40					45				
15	Lys	Glu	Arg	Ala	Leu	His	Lys	Ala	Pro	Tyr	Tyr	Phe	Leu	Leu	Asp	Leu	
		50					55					60					
	Cys	Leu	Ala	Asp	Gly	Ile	Arg	Ser	Ala	Val	Cys	Phe	Pro	Phe	Val	Leu	
	65					70					75					80	
	Ala	Ser	Val	Arg	His	Gly	Ser	Ser	Trp	Thr	Phe	Ser	Ala	Leu	Ser	Cys	
				85						90					95		
20	Lys	Ile	Val	Ala	Phe	Met	Ala	Val	Leu	Phe	Cys	Phe	His	Ala	Ala	Phe	
				100					105					110			
	Met	Leu	Phe	Cys	Ile	Ser	Val	Thr	Arg	Tyr	Met	Ala	Ile	Ala	His	His	
		115						120					125				
25	Arg	Phe	Tyr	Ala	Lys	Arg	Met	Thr	Leu	Trp	Thr	Cys	Ala	Ala	Val	Ile	
		130					135					140					
	Cys	Met	Ala	Trp	Thr	Leu	Ser	Val	Ala	Met	Ala	Phe	Pro	Pro	Val	Phe	
	145					150					155				160		
	Asp	Val	Gly	Thr	Tyr	Lys	Phe	Ile	Arg	Glu	Glu	Asp	Gln	Cys	Ile	Phe	
				165						170				175			
30	Glu	His	Arg	Tyr	Phe	Lys	Ala	Asn	Asp	Thr	Leu	Gly	Phe	Met	Leu	Met	
				180					185					190			
	Leu	Ala	Val	Leu	Met	Ala	Ala	Thr	His	Ala	Val	Tyr	Gly	Lys	Leu	Leu	
			195					200					205				
35	Leu	Phe	Glu	Tyr	Arg	His	Arg	Lys	Met	Lys	Pro	Val	Gln	Met	Val	Pro	
		210					215					220					
	Ala	Ile	Ser	Gln	Asn	Trp	Thr	Phe	His	Gly	Pro	Gly	Ala	Thr	Gly	Gln	
	225					230					235				240		

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	Ala	Ala	Ala	Asn	Trp	Ile	Ala	Gly	Phe	Gly	Arg	Gly	Pro	Met	Pro	Pro	245	250	255
	Thr	Leu	Leu	Gly	Ile	Arg	Gln	Asn	Gly	His	Ala	Ala	Ser	Arg	Arg	Leu	260	265	270
5	Leu	Gly	Met	Asp	Glu	Val	Lys	Gly	Glu	Lys	Gln	Leu	Gly	Arg	Met	Phe	275	280	285
	Tyr	Ala	Ile	Thr	Leu	Leu	Phe	Leu	Leu	Leu	Trp	Ser	Pro	Tyr	Ile	Val	290	295	300
10	Ala	Cys	Tyr	Trp	Arg	Val	Phe	Val	Lys	Ala	Cys	Ala	Val	Pro	His	Arg	305	310	315
	Tyr	Leu	Ala	Thr	Ala	Val	Trp	Met	Ser	Phe	Ala	Gln	Ala	Ala	Val	Asn	325	330	335
	Pro	Ile	Val	Cys	Phe	Leu	Leu	Asn	Lys	Asp	Leu	Lys	Lys	Cys	Leu	Thr	340	345	350
15	Thr	His	Ala	Pro	Cys	Trp	Gly	Thr	Gly	Gly	Ala	Pro	Ala	Pro	Arg	Glu	355	360	365
	Pro	Tyr	Cys	Val	Met												370		

(24) INFORMATION FOR SEQ ID NO:23:

20 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

	ATGGCTTTGG	AACAGAACCA	GTCAACAGAT	TATTATTATG	AGGAAAATGA	AATGAATGGC	60
	ACTTATGACT	ACAGTCAATA	TGAATTGATC	TGTATCAAAG	AAGATGTCAG	AGAATTTGCA	120
	AAAGTTTTCC	TCCCTGTATT	CCTCACAATA	GCTTTCGTCA	TTGGACTTGC	AGGCAATTCC	180
30	ATGGTAGTGG	CAATTTATGC	CTATTACAAG	AAACAGAGAA	CCAAAACAGA	TGTGTACATC	240
	CTGAATTTGG	CTGTAGCAGA	TTTACTCCTT	CTATTCACTC	TGCCTTTTTG	GGCTGTTAAT	300
	GCAGTTCATG	GGTGGGTTTT	AGGGAAAATA	ATGTGCAAAA	TAAGTTCAGC	CTTGTACACA	360
	CTAAACTTTG	TCTCTGGAAT	GCAGTTTCTG	GCTTGCATCA	GCATAGACAG	ATATGTGGCA	420
	GTAACATAATG	TCCCCAGCCA	ATCAGGAGTG	GGAAAACCAT	GCTGGATCAT	CTGTTTCTGT	480

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GTCTGGATGG CTGCCATCTT GCTGAGCATA CCCCAGCTGG TTTTATATAC AGTAAATGAC 540
 AATGCTAGGT GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT 600
 CAAATGCTAG AGATCTGCAT TGGATTTGTA GTACCCTTTC TTATTATGGG GGTGTGCTAC 660
 TTTATCACGG CAAGGACACT CATGAAGATG CCAAACATTA AAATATCTCG ACCCCTAAAA 720
 5 GTTCTGCTCA CAGTCGTTAT AGTTTTCATT GTCACTCAAC TGCCTTATAA CATTGTCAAG 780
 TTCTGCCGAG CCATAGACAT CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC 840
 ATGGACATCG CCATCCAAGT CACAGAAAGC ATTGCACTCT TTCACAGCTG CCTCAACCCA 900
 ATCCTTTATG TTTTATGGG AGCATCTTTC AAAAAGTACG TTATGAAAGT GGCCAAGAAA 960
 TATGGGTCCT GGAGAAGACA GAGACAAAGT GTGGAGGAGT TTCCTTTTGA TTCTGAGGGT 1020
 10 CCTACAGAGC CAACCAAGTAC TTTTAGCATT TAA 1053

(25) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 15 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

20 Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
 1 5 10 15
 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
 20 25 30
 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
 35 40 45
 25 Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
 50 55 60
 Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
 65 70 75 80
 30 Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe
 85 90 95
 Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
 100 105 110
 Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln

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	115	120	125
	Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val		
	130	135	140
5	Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys		
	145	150	155
	Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr		
		165	170
	Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu		
		180	185
10	Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly		
		195	200
	Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala		
		210	215
15	Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys		
		225	230
	Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr		
		245	250
	Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile		
		260	265
20	Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr		
		275	280
	Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val		
		290	295
25	Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys		
		305	310
	Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe		
		315	320
		325	330
	Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile		
		340	345
			350

30 (26) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1116 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

ATGCCAGGAA ACGCCACCCC AGTGACCACC ACTGCCCCGT GGGCCTCCCT GGGCCTCTCC   60
GCCAAGACCT GCAACAACGT GTCCTTCGAA GAGAGCAGGA TAGTCCTGGT CGTGGTGTAC   120
AGCGCGGTGT GCACGCTGGG GGTGCCGGCC AACTGCCTGA CTGCGTGGCT GGCCTGCTG   180
5  CAGGTACTGC AGGGCAACGT GCTGGCCGTC TACCTGCTCT GCCTGGCACT CTGCGAACTG   240
CTGTACACAG GCACGCTGCC ACTCTGGGTC ATCTATATCC GCAACCAGCA CCGCTGGACC   300
CTAGGCCTGC TGGCCTCGAA GGTGACCGCC TACATCTTCT TCTGCAACAT CTACGTCAGC   360
ATCCTCTTCC TGTGCTGCAT CTCCTGCGAC CGCTTCGTGG CCGTGGTGTA CGCGCTGGAG   420
AGTCGGGGCC GCCGCCGCCG GAGGACCGCC ATCCTCATCT CCGCCTGCAT CTTTCATCTC   480
10  GTCGGGATCG TTCACTACCC GGTGTTCCAG ACGGAAGACA AGGAGACCTG CTTTGACATG   540
CTGCAGATGG ACAGCAGGAT TGCCGGGTAC TACTACGCCA GGTTCACCGT TGGCTTTGCC   600
ATCCCTCTCT CCATCATCGC CTTACCAAC CACCGGATT TCAAGAGCAT CAAGCAGAGC   660
ATGGGCTTAA GCGCTGCCCA GAAGGCCAAG GTGAAGCACT CGGCCATCGC GGTGGTTGTC   720
ATCTTCCTAG TCTGCTTCGC CCCGTACCAC CTGGTTCTCC TCGTCAAAGC CGCTGCCTTT   780
15  TCCTACTACA GAGGAGACAG GAACGCCATG TGCGGCTTGG AGGAAAGGCT GTACACAGCC   840
TCTGTGGTGT TTCTGTGCCT GTCCACGGTG AACGGCGTGG CTGACCCCAT TATCTACGTG   900
CTGGCCACGG ACCATTCCCG CCAAGAAGTG TCCAGAATCC ATAAGGGGTG GAAAGAGTGG   960
TCCATGAAGA CAGACGTCAC CAGGCTCACC CACAGCAGGG ACACCGAGGA GCTGCAGTCG  1020
CCCGTGGCCC TTGCAGACCA CTACACCTTC TCCAGGCCCG TGCACCCACC AGGGTCACCA  1080
20  TGCCCTGCAA AGAGGCTGAT TGAGGAGTCC TGCTGA                               1116

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(28) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser
30  1                      5                      10                      15

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	Leu	Gly	Leu	Ser	Ala	Lys	Thr	Cys	Asn	Asn	Val	Ser	Phe	Glu	Glu	Ser	
				20					25					30			
	Arg	Ile	Val	Leu	Val	Val	Val	Tyr	Ser	Ala	Val	Cys	Thr	Leu	Gly	Val	
			35					40					45				
5	Pro	Ala	Asn	Cys	Leu	Thr	Ala	Trp	Leu	Ala	Leu	Leu	Gln	Val	Leu	Gln	
		50					55					60					
	Gly	Asn	Val	Leu	Ala	Val	Tyr	Leu	Leu	Cys	Leu	Ala	Leu	Cys	Glu	Leu	
	65					70					75					80	
10	Leu	Tyr	Thr	Gly	Thr	Leu	Pro	Leu	Trp	Val	Ile	Tyr	Ile	Arg	Asn	Gln	
					85					90					95		
	His	Arg	Trp	Thr	Leu	Gly	Leu	Leu	Ala	Ser	Lys	Val	Thr	Ala	Tyr	Ile	
				100					105						110		
	Phe	Phe	Cys	Asn	Ile	Tyr	Val	Ser	Ile	Leu	Phe	Leu	Cys	Cys	Ile	Ser	
			115					120					125				
15	Cys	Asp	Arg	Phe	Val	Ala	Val	Val	Tyr	Ala	Leu	Glu	Ser	Arg	Gly	Arg	
		130					135					140					
	Arg	Arg	Arg	Arg	Thr	Ala	Ile	Leu	Ile	Ser	Ala	Cys	Ile	Phe	Ile	Leu	
	145					150					155					160	
20	Val	Gly	Ile	Val	His	Tyr	Pro	Val	Phe	Gln	Thr	Glu	Asp	Lys	Glu	Thr	
					165					170					175		
	Cys	Phe	Asp	Met	Leu	Gln	Met	Asp	Ser	Arg	Ile	Ala	Gly	Tyr	Tyr	Tyr	
				180					185					190			
	Ala	Arg	Phe	Thr	Val	Gly	Phe	Ala	Ile	Pro	Leu	Ser	Ile	Ile	Ala	Phe	
				195				200					205				
25	Thr	Asn	His	Arg	Ile	Phe	Arg	Ser	Ile	Lys	Gln	Ser	Met	Gly	Leu	Ser	
		210					215					220					
	Ala	Ala	Gln	Lys	Ala	Lys	Val	Lys	His	Ser	Ala	Ile	Ala	Val	Val	Val	
	225					230					235					240	
30	Ile	Phe	Leu	Val	Cys	Phe	Ala	Pro	Tyr	His	Leu	Val	Leu	Leu	Val	Lys	
					245					250					255		
	Ala	Ala	Ala	Phe	Ser	Tyr	Tyr	Arg	Gly	Asp	Arg	Asn	Ala	Met	Cys	Gly	
				260					265					270			
	Leu	Glu	Glu	Arg	Leu	Tyr	Thr	Ala	Ser	Val	Val	Phe	Leu	Cys	Leu	Ser	
			275					280					285				
35	Thr	Val	Asn	Gly	Val	Ala	Asp	Pro	Ile	Ile	Tyr	Val	Leu	Ala	Thr	Asp	
		290					295						300				

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His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp
 305 310 315 320
 Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu
 325 330 335
 5 Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg
 340 345 350
 Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu
 355 360 365
 10 Glu Ser Cys
 370

(28) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGGCGAACT ATAGCCATGC AGCTGACAAC ATTTTGCAAA ATCTCTCGCC TCTAACAGCC 60
 20 TTTCTGAAAC TGACTTCCTT GGGTTTCATA ATAGGAGTCA GCGTGGTGGG CAACCTCCTG 120
 ATCTCCATTT TGCTAGTGAA AGATAAGACC TTGCATAGAG CACCTTACTA CTTCCTGTTG 180
 GATCTTTGCT GTTCAGATAT CCTCAGATCT GCAATTGTGT TCCCATTTGT GTTCAACTCT 240
 GTCAAAAATG GCTCTACCTG GACTTATGGG ACTCTGACTT GCAAAGTGAT TGCCTTTCTG 300
 GGGGTTTTGT CCTGTTTCCA CACTGCTTTC ATGCTCTTCT GCATCAGTGT CACCAGATAC 360
 25 TTAGCTATCG CCCATCACCG CTTCTATACA AAGAGGCTGA CCTTTTGGAC GTGTCTGGCT 420
 GTGATCTGTA TGGTGTGGAC TCTGTCTGTG GCCATGGCAT TTCCCCCGGT TTTAGACGTG 480
 GGCACTTACT CATTCAATTAG GGAGGAAGAT CAATGCACCT TCCAACACCG CTCCTTCAGG 540
 GCTAATGATT CCTTAGGATT TATGCTGCTT CTGCTCTCA TCCTCCTAGC CACACAGCTT 600
 GTCTACCTCA AGCTGATATT TTTCGTCCAC GATCGAAGAA AAATGAAGCC AGTCCAGTTT 660
 30 GTAGCAGCAG TCAGCCAGAA CTGGACTTTT CATGGTCTCTG GAGCCAGTGG CCAGGCAGCT 720
 GCCAATTGGC TAGCAGGATT TGAAGGGGT CCCACACCAC CCACCTTGCT GGGCATCAGG 780
 CAAAATGCAA ACACCACAGG CAGAAGAAGG CTATTGGTCT TAGACGAGTT CAAAATGGAG 840

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AAAAGAATCA GCAGAATGTT CTATATAATG ACTTTTCTGT TTCTAACCTT GTGGGGCCCC 900
 TACCTGGTGG CCTGTTATTG GAGAGTTTTT GCAAGAGGGC CTGTAGTACC AGGGGGATTT 960
 CTAACAGCTG CTGTCTGGAT GAGTTTTGCC CAAGCAGGAA TCAATCCTTT TGTCTGCATT 1020
 TTCTCAAACA GGGAGCTGAG GCGCTGTTTC AGCACAACCC TTCTTTACTG CAGAAAATCC 1080
 5 AGGTTACCAA GGGAACCTTA CTGTGTTATA TGA 1113

(29) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 10 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

15 Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
 1 5 10 15
 Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
 20 25 30
 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45
 20 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60
 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80
 25 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95
 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
 100 105 110
 Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
 115 120 125
 30 Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
 130 135 140
 Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
 145 150 155 160
 Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His

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		165		170		175
	Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala					
		180		185		190
5	Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe					
		195		200		205
	Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val					
		210		215		220
	Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala					
		225		230		235 240
10	Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu					
		245		250		255
	Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu					
		260		265		270
15	Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr					
		275		280		285
	Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala					
		290		295		300
	Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe					
		305		310		315 320
20	Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro					
		325		330		335
	Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr					
		340		345		350
25	Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys					
		355		360		365
	Val Ile					
	370					

(30) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGCAGGTCC CGAACAGCAC CGGCCCGGAC AACGCGACGC TGCAGATGCT GCGGAACCCG 60

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GCGATCGCGG TGGCCCTGCC CGTGGTGTAC TCGCTGGTGG CGGCGGTCAG CATCCCGGGC 120
AACCTCTTCT CTCTGTGGGT GCTGTGCCGG CGCATGGGGC CCAGATCCCC GTCGGTCATC 180
TTCATGATCA ACCTGAGCGT CACGGACCTG ATGCTGGCCA GCGTGTGACC TTTCCAAATC 240
TACTACCATT GCAACCGCCA CCACTGGGTA TTCGGGGTGC TGCTTTGCAA CGTGGTGACC 300
5 GTGGCCTTTT ACGCAAACAT GTATTCCAGC ATCCTCACCA TGACCTGTAT CAGCGTGGAG 360
CGCTTCCTGG GGGTCCTGTA CCCGCTCAGC TCCAAGCGCT GGCGCCGCCG TCGTTACGCG 420
GTGGCCGCGT GTGCAGGGAC CTGGCTGCTG CTCCTGACCG CCCTGTGCCC GCTGGCGCGC 480
ACCGATCTCA CCTACCCGGT GCACGCCCTG GGCATCATCA CCTGCTTCGA CGTCCCTCAAG 540
TGGACGATGC TCCCCAGCGT GGCCATGTGG GCCGTGTTCC TCTTCACCAT CTTTCATCCTG 600
10 CTGTTCTCTCA TCCCGTTTCGT GATCACCGTG GCTTGTTACA CGGCCACCAT CCTCAAGCTG 660
TTGCGCACGG AGGAGGCGCA CGGCCGGGAG CAGCGGAGGC GCGCGGTGGG CCTGGCCGCG 720
GTGGTCTTGC TGGCCTTTGT CACCTGCTTC GCCCCAACA ACTTCGTGCT CCTGGCGCAC 780
ATCGTGAGCC GCCTGTTCTA CGCAAGAGC TACTACCAG TGTACAAGCT CACGCTGTGT 840
CTCAGCTGCC TCAACAACTG TCTGGACCCG TTTGTTTATT ACTTTGCGTC CCGGGAATTC 900
15 CAGCTGCGCC TGCGGGAATA TTTGGGCTGC CGCCGGGTGC CCAGAGACAC CCTGGACACG 960
CGCCGCGAGA GCCTCTTCTC CGCCAGGACC ACGTCCGTGC GCTCCGAGGC CGGTGCGCAC 1020
CCTGAAGGGA TGGAGGGAGC CACCAGGCCC GGCCTCCAGA GGCAGGAGAG TGTGTTCTGA 1080

(31) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met
1 5 10 15

Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
20 25 30

- 30 Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu

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	35	40	45
	Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn		
	50	55	60
5	Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile		
	65	70	75 80
	Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys		
		85	90 95
	Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu		
		100	105 110
10	Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro		
		115	120 125
	Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys		
		130	135 140
15	Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg		
		145	150 155 160
	Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe		
		165	170 175
	Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val		
		180	185 190
20	Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile		
		195	200 205
	Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu		
		210	215 220
25	Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala		
		225	230 235 240
	Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val		
		245	250 255
	Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr		
		260	265 270
30	His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu		
		275	280 285
	Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu		
		290	295 300
35	Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr		
		305	310 315 320
	Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu		
		325	330 335

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Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
 340 345 350

Gln Arg Gln Glu Ser Val Phe
 355

5 (32) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGAGCGTC CCTGGGAGGA CAGCCCAGGC CCGGAGGGGG CAGCTGAGGG CTCGCCTGTG 60
 CCAGTCGCCG CCGGGGCGCG CTCCGGTGCC GCGGCGAGTG GCACAGGCTG GCAGCCATGG 120
 15 GCTGAGTGCC CGGGACCCAA GGGGAGGGGG CAACTGCTGG CGACCGCCGG CCCTTTGCGT 180
 CGCTGGCCCC CCCCCTCGCC TGCCAGCTCC AGCCCCGCCC CCGGAGCGGC GTCCGCTCAC 240
 TCGGTTCAAG GCAGCGCGAC TCGGGGTGGC GCACGACCAG GGCAGAGACC TTGGGGCGCG 300
 CGGCCCATGG AGTCGGGGCT GCTGCGGCCG GCGCCGTGA GCGAGGTCAT CGTCCTGCAT 360
 TACAATAACA CCGGCAAGCT CCGCGGTGCG AGCTACCAGC CGGGTGCCCG CCTGCGCGCC 420
 20 GACGCCGTGG TGTGCCTGGC GGTGTGCGCC TTCATCGTGC TAGAGAATCT AGCCGTGTTG 480
 TTGGTGCTCG GACGCCACCC GCGCTTCCAC GCTCCCATGT TCCTGCTCCT GGGCAGCCTC 540
 ACGTTGTGCG ATCTGCTGGC AGGCGCCGCC TACGCCGCCA ACATCCTACT GTCGGGGCCG 600
 CTCACGCTGA AACTGTCCCC CCGCTCTGCG TTCGCACGGG AGGGAGGCGT CTTCGTGGCA 660
 CTCACTGCGT CCGTGCTGAG CCTCCTGGCC ATCGCGCTGG AGCGCAGCCT CACCATGGCG 720
 25 CGCAGGGGGC CCGCGCCCGT CTCCAGTCGG GGGCGCACGC TGGCGATGGC AGCCGCGGCC 780
 TGGGGCGTGT CGCTGCTCCT CCGGCTCCTG CCAGCGCTGG GCTGGAATTG CCTGGGTGCG 840
 CTGGACGCTT GCTCCACTGT CTTGCCGCTC TACGCCAAGG CCTACGTGCT CTTCTGCGTG 900
 CTCGCCTTCG TGGGCATCCT GGCCGCGATC TGTGCACTCT ACGCGCGCAT CTACTGCCAG 960
 GTACGCGCCA ACGCGCGGCG CCTGCCGGCA CGGCCCGGGA CTGCGGGGAC CACCTCGACC 1020
 30 CGGGCGCGTC GCAAGCCGCG CTCTCTGGCC TTGCTGCGCA CGCTCAGCGT GGTGCTCCTG 1080

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GCCTTTGTGG CATGTTGGGG CCCCCTCTTC CTGCTGCTGT TGCTCGACGT GGCCTGCCCCG 1140
GCGCGCACCT GTCCTGTACT CCTGCAGGCC GATCCCTTCC TGGGACTGGC CATGGCCAAC 1200
TCACTTCTGA ACCCCATCAT CTACACGCTC ACCAACCGCG ACCTGCGCCA CGCGCTCCTG 1260
CGCCTGGTCT GCTGCGGACG CCACTCCTGC GGCAGAGACC CGAGTGGCTC CCAGCAGTCG 1320
5 GCGAGCGCGG CTGAGGCTTC CGGGGGCCTG CGCCGCTGCC TGCCCCCGGG CCTTGATGGG 1380
AGCTTCAGCG GCTCGGAGCG CTCATCGCCC CAGCGCGACG GGCTGGACAC CAGCGGCTCC 1440
ACAGGCAGCC CCGGTGCACC CACAGCCGCC CGGACTCTGG TATCAGAACC GGCTGCAGAC 1500
TGA 1503

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(33) INFORMATION FOR SEQ ID NO:32:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu
1           5           10           15
Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala
20          20          25          30
Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly
35          40          45
Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala
50          55          60
25 Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His
65          70          75          80
Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg
85          90          95
30 Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro
100         105         110
Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg
115         120         125
Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val
130         135         140

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	Cys	Leu	Ala	Val	Cys	Ala	Phe	Ile	Val	Leu	Glu	Asn	Leu	Ala	Val	Leu	145	150	155	160
	Leu	Val	Leu	Gly	Arg	His	Pro	Arg	Phe	His	Ala	Pro	Met	Phe	Leu	Leu	165	170	175	
5	Leu	Gly	Ser	Leu	Thr	Leu	Ser	Asp	Leu	Leu	Ala	Gly	Ala	Ala	Tyr	Ala	180	185	190	
	Ala	Asn	Ile	Leu	Leu	Ser	Gly	Pro	Leu	Thr	Leu	Lys	Leu	Ser	Pro	Ala	195	200	205	
10	Leu	Trp	Phe	Ala	Arg	Glu	Gly	Gly	Val	Phe	Val	Ala	Leu	Thr	Ala	Ser	210	215	220	
	Val	Leu	Ser	Leu	Leu	Ala	Ile	Ala	Leu	Glu	Arg	Ser	Leu	Thr	Met	Ala	225	230	235	240
	Arg	Arg	Gly	Pro	Ala	Pro	Val	Ser	Ser	Arg	Gly	Arg	Thr	Leu	Ala	Met	245	250	255	
15	Ala	Ala	Ala	Ala	Trp	Gly	Val	Ser	Leu	Leu	Leu	Gly	Leu	Leu	Pro	Ala	260	265	270	
	Leu	Gly	Trp	Asn	Cys	Leu	Gly	Arg	Leu	Asp	Ala	Cys	Ser	Thr	Val	Leu	275	280	285	
20	Pro	Leu	Tyr	Ala	Lys	Ala	Tyr	Val	Leu	Phe	Cys	Val	Leu	Ala	Phe	Val	290	295	300	
	Gly	Ile	Leu	Ala	Ala	Ile	Cys	Ala	Leu	Tyr	Ala	Arg	Ile	Tyr	Cys	Gln	305	310	315	320
	Val	Arg	Ala	Asn	Ala	Arg	Arg	Leu	Pro	Ala	Arg	Pro	Gly	Thr	Ala	Gly	325	330	335	
25	Thr	Thr	Ser	Thr	Arg	Ala	Arg	Arg	Lys	Pro	Arg	Ser	Leu	Ala	Leu	Leu	340	345	350	
	Arg	Thr	Leu	Ser	Val	Val	Leu	Leu	Ala	Phe	Val	Ala	Cys	Trp	Gly	Pro	355	360	365	
30	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Asp	Val	Ala	Cys	Pro	Ala	Arg	Thr	Cys	370	375	380	
	Pro	Val	Leu	Leu	Gln	Ala	Asp	Pro	Phe	Leu	Gly	Leu	Ala	Met	Ala	Asn	385	390	395	400
	Ser	Leu	Leu	Asn	Pro	Ile	Ile	Tyr	Thr	Leu	Thr	Asn	Arg	Asp	Leu	Arg	405	410	415	
35	His	Ala	Leu	Leu	Arg	Leu	Val	Cys	Cys	Gly	Arg	His	Ser	Cys	Gly	Arg	420	425	430	
	Asp	Pro	Ser	Gly	Ser	Gln	Gln	Ser	Ala	Ser	Ala	Ala	Glu	Ala	Ser	Gly				

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435 440 445

Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly
 450 455 460

5 Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser
 465 470 475 480

Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu
 485 490 495

Pro Ala Ala Asp
 500

10 (34) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1029 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGCAAGCCG TCGACAATCT CACCTCTGCG CCTGGGAACA CCAGTCTGTG CACCAGAGAC 60

TACAAAATCA CCCAGGTCCT CTCCCACTG CTCTACACTG TCCTGTTTTT TGTGACTT 120

20 ATCACAAATG GCCTGGCGAT GAGGATTTTC TTCAAAATCC GGAGTAAATC AAACCTTTAT 180

ATTTTTCTTA AGAACACAGT CATTTCTGAT CTTCTCATGA TTCTGACTTT TCCATTCAAA 240

ATTCTTAGTG ATGCCAACT GGGAACAGGA CCACTGAGAA CTTTGTGTG TCAAGTTACC 300

TCCGTCATAT TTTATTTTAC AATGTATATC AGTATTTTCT TCCTGGGACT GATAACTATC 360

GATCGCTACC AGAAGACCAC CAGGCCATTT AAAACATCCA ACCCCAAAAA TCTCTTGGGG 420

25 GCTAAGATTC TCTCTGTTGT CATCTGGGCA TTCATGTTCT TACTCTCTTT GCCTAACATG 480

ATTCTGACCA ACAGGCAGCC GAGAGACAAG AATGTGAAGA AATGCTCTTT CCTTAAATCA 540

GAGTTCGGTC TAGTCTGGCA TGAAATAGTA AATTACATCT GTCAAGTCAT TTTCTGGATT 600

AATTTCTTAA TTGTTATTGT ATGTTATACA CTCATTACAA AAGAACTGTA CCGGTCATAC 660

GTAAGAACGA GGGGTGTAGG TAAAGTCCCC AGGAAAAAGG TGAACGTCAA AGTTTTCATT 720

30 ATCATGCTG TATTCTTTAT TTGTTTGT CTTTCCATT TTGCCGAAT TCCTTACACC 780

CTGAGCCAAA CCCGGGATGT CTTTGACTGC ACTGCTGAAA ATACTCTGTT CTATGTGAAA 840

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GAGAGCACTC TGTGGTTAAC TTCCTTAAAT GCATGCCTGG ATCCGTTTAT CTATTTTTTC 900
 CTTTGCAAGT CCTTCAGAAA TTCCTTGATA AGTATGCTGA AGTGCCCCAA TTCTGCAACA 960
 TCTCTGTCCC AGGACAATAG GAAAAAGAA CAGGATGGTG GTGACCCAAA TGAAGAGACT 1020
 CCAATGTAA 1029

5 (35) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 10 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

	Met	Gln	Ala	Val	Asp	Asn	Leu	Thr	Ser	Ala	Pro	Gly	Asn	Thr	Ser	Leu	
	1				5					10					15		
15	Cys	Thr	Arg	Asp	Tyr	Lys	Ile	Thr	Gln	Val	Leu	Phe	Pro	Leu	Leu	Tyr	
				20					25					30			
	Thr	Val	Leu	Phe	Phe	Val	Gly	Leu	Ile	Thr	Asn	Gly	Leu	Ala	Met	Arg	
				35				40					45				
20	Ile	Phe	Phe	Gln	Ile	Arg	Ser	Lys	Ser	Asn	Phe	Ile	Ile	Phe	Leu	Lys	
		50					55				60						
	Asn	Thr	Val	Ile	Ser	Asp	Leu	Leu	Met	Ile	Leu	Thr	Phe	Pro	Phe	Lys	
	65				70					75						80	
	Ile	Leu	Ser	Asp	Ala	Lys	Leu	Gly	Thr	Gly	Pro	Leu	Arg	Thr	Phe	Val	
				85					90					95			
25	Cys	Gln	Val	Thr	Ser	Val	Ile	Phe	Tyr	Phe	Thr	Met	Tyr	Ile	Ser	Ile	
				100					105					110			
	Ser	Phe	Leu	Gly	Leu	Ile	Thr	Ile	Asp	Arg	Tyr	Gln	Lys	Thr	Thr	Arg	
			115				120						125				
30	Pro	Phe	Lys	Thr	Ser	Asn	Pro	Lys	Asn	Leu	Leu	Gly	Ala	Lys	Ile	Leu	
		130				135						140					
	Ser	Val	Val	Ile	Trp	Ala	Phe	Met	Phe	Leu	Leu	Ser	Leu	Pro	Asn	Met	
	145				150					155					160		
	Ile	Leu	Thr	Asn	Arg	Gln	Pro	Arg	Asp	Lys	Asn	Val	Lys	Lys	Cys	Ser	
				165					170						175		
35	Phe	Leu	Lys	Ser	Glu	Phe	Gly	Leu	Val	Trp	His	Glu	Ile	Val	Asn	Tyr	

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	180	185	190
	Ile Cys Gln Val Ile Phe Trp	Ile Asn Phe Leu Ile	Val Ile Val Cys
	195	200	205
5	Tyr Thr Leu Ile Thr Lys	Glu Leu Tyr Arg Ser Tyr	Val Arg Thr Arg
	210	215	220
	Gly Val Gly Lys Val Pro Arg	Lys Lys Val Asn Val	Lys Val Phe Ile
	225	230	235 240
	Ile Ile Ala Val Phe Phe Ile	Cys Phe Val Pro Phe His	Phe Ala Arg
	245	250	255
10	Ile Pro Tyr Thr Leu Ser Gln	Thr Arg Asp Val Phe Asp	Cys Thr Ala
	260	265	270
	Glu Asn Thr Leu Phe Tyr Val	Lys Glu Ser Thr Leu Trp	Leu Thr Ser
	275	280	285
15	Leu Asn Ala Cys Leu Asp Pro	Phe Ile Tyr Phe Phe	Leu Cys Lys Ser
	290	295	300
	Phe Arg Asn Ser Leu Ile Ser	Met Leu Lys Cys Pro	Asn Ser Ala Thr
	305	310	315 320
	Ser Leu Ser Gln Asp Asn Arg	Lys Lys Glu Gln Asp	Gly Gly Asp Pro
	325	330	335
20	Asn Glu Glu Thr Pro Met		
	340		

(36) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

30	ATGTCGGTCT GCTACCGTCC CCCAGGGAAC GAGACACTGC TGAGCTGGAA GACTTCGCGG	60
	GCCACAGGCA CAGCCTTCCT GCTGCTGGCG GCGTGTCTGG GGCTGCCTGG CAACGGCTTC	120
	GTGGTGTGGA GCTTGGCGGG CTGGCGGCCT GCACGGGGGC GACCGCTGGC GGCCACGCTT	180
	GTGCTGCACC TGGCGCTGGC CGACGGCGCG GTGCTGTCTG TCACGCCGCT CTTTGTGGCC	240
	TTCCTGACCC GGCAGGCCTG GCCGCTGGGC CAGGCGGGCT GCAAGGCGGT GTACTACGTG	300

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TGC GCGCTCA GCATGTACGC CAGCGTGCTG CTCACCGGCC TGCTCAGCCT GCAGCGCTGC 360
 CTCGCAGTCA CCCGCCCTT CCTGGCGCCT CGGCTGCGCA GCCCGGCCCT GGCCCGCCGC 420
 CTGCTGCTGG CCGTCTGGCT GGCCGCCCTG TTGCTCGCCG TCCCGGCCGC CGTCTACCGC 480
 CACCTGTGGA GGGACCGCGT ATGCCAGCTG TGCCACCCGT CGCCGGTCCA CGCCGCCGCC 540
 5 CACCTGAGCC TGGAGACTCT GACCGCTTTC GTGCTTCCTT TCGGGCTGAT GCTCGGCTGC 600
 TACAGCGTGA CGCTGGCACG GCTGCGGGG GCCCGCTGGG GCTCCGGGCG GCACGGGGCG 660
 CGGGTGGGCC GGCTGGTGAG CGCCATCGTG CTTGCCTTCG GCTTGCTCTG GGCCCCCTAC 720
 CACGCAGTCA ACCTTCTGCA GGCGGTCGCA GCGCTGGCTC CACCGGAAGG GGCCTTGGCG 780
 AAGCTGGGCG GAGCCGGCCA GGCGGCGCA GCGGGAATA CGGCCTTGGC CTTCTTCACT 840
 10 TCTAGCGTCA ACCCGGTGCT CTACGTCTTC ACCGCTGGAG ATCTGCTGCC CCGGGCAGGT 900
 CCCCGTTTCC TCACGCGGCT CTTCAAGGC TCTGGGAGG CCCGAGGGG CGGCCGCTCT 960
 AGGGAAGGGA CCATGGAGCT CCGAACTACC CCTCAGCTGA AAGTGGTGGG GCAGGGCCGC 1020
 GGCAATGGAG ACCCGGGGGG TGGGATGGAG AAGGACGGTC CGGAATGGGA CCTTTGA 1077

(37) INFORMATION FOR SEQ ID NO:36:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp
 1 5 10 15
 Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu
 25 20 25 30
 Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp
 35 40 45
 Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu
 50 55 60
 30 Ala Leu Ala Asp Gly Ala Val Leu Leu Leu Thr Pro Leu Phe Val Ala
 65 70 75 80
 Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala

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	85	90	95
	Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr		
	100	105	110
5	Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu		
	115	120	125
	Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala		
	130	135	140
	Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg		
	145	150	155
10	His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val		
	165	170	175
	His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu		
	180	185	190
15	Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu		
	195	200	205
	Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg		
	210	215	220
	Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr		
	225	230	235
20	His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu		
	245	250	255
	Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly		
	260	265	270
25	Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr		
	275	280	285
	Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu		
	290	295	300
	Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser		
	305	310	315
30	Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val		
	325	330	335
	Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Gly Met Glu Lys Asp		
	340	345	350
35	Gly Pro Glu Trp Asp Leu		
	355		

(38) INFORMATION FOR SEQ ID NO:37:

- 45 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1005 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGCTGGGGA TCATGGCATG GAATGCAACT TGCAAAACT GGCTGGCAGC AGAGGCTGCC 60
CTGGAAAAGT ACTACCTTTC CATTTTAT GGGATTGAGT TCGTTGTGGG AGTCCTTGGA 120
10 AATACCATTG TTGTTTACGG CTACATCTTC TCTCTGAAGA ACTGGAACAG CAGTAATATT 180
TATCTCTTTA ACCTCTCTGT CTCTGACTTA GCTTTTCTGT GCACCCTCCC CATGCTGATA 240
AGGAGTTATG CCAATGGAAA CTGGATATAT GGAGACGTGC TCTGCATAAG CAACCGATAT 300
GTGCTTCATG CCAACCTCTA TACCAGCATT CTCTTTCTCA CTTTATCAG CATAGATCGA 360
TACTTGATAA TTAAGTATCC TTCCGAGAA CACCTTCTGC AAAAGAAAGA GTTGCTATT 420
15 TTAATCTCCT TGGCCATTG GGTTTAGTA ACCTTAGAGT TACTACCCAT ACTTCCCCTT 480
ATAAATCCTG TTATAACTGA CAATGGCACC ACCTGTAATG ATTTTGCAAG TTCTGGAGAC 540
CCCAACTACA ACCTCATTTA CAGCATGTGT CTAACACTGT TGGGGTTCCT TATTCCTCTT 600
TTTGTGATGT GTTCTTTTA TTACAAGATT GCTCTCTTCC TAAAGCAGAG GAATAGGCAG 660
GTTGCTACTG CTCTGCCCT TGAAAAGCCT CTCAACTGG TCATCATGGC AGTGGTAATC 720
20 TTCTCTGTGC TTTTACACC CTATCACGTC ATGCGGAATG TGAGGATCGC TTCACGCCTG 780
GGGAGTTGGA AGCAGTATCA GTGCACTCAG GTCGTCATCA ACTCCTTTTA CATTGTGACA 840
CGGCCTTTGG CCTTTCTGAA CAGTGTATC AACCTGTCT TCTATTTTCT TTGGGAGAT 900
CACTTCAGGG ACATGCTGAT GAATCAACTG AGACACAACT TCAAATCCCT TACATCCTTT 960
AGCAGATGGG CTCATGAACT CCTACTTTCA TTCAGAGAAA AGTGA 1005

25 (39) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

30

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	Met	Leu	Gly	Ile	Met	Ala	Trp	Asn	Ala	Thr	Cys	Lys	Asn	Trp	Leu	Ala	
	1				5					10					15		
5	Ala	Glu	Ala	Ala	Leu	Glu	Lys	Tyr	Tyr	Leu	Ser	Ile	Phe	Tyr	Gly	Ile	
				20					25					30			
	Glu	Phe	Val	Val	Gly	Val	Leu	Gly	Asn	Thr	Ile	Val	Val	Tyr	Gly	Tyr	
			35					40					45				
	Ile	Phe	Ser	Leu	Lys	Asn	Trp	Asn	Ser	Ser	Asn	Ile	Tyr	Leu	Phe	Asn	
		50					55					60					
10	Leu	Ser	Val	Ser	Asp	Leu	Ala	Phe	Leu	Cys	Thr	Leu	Pro	Met	Leu	Ile	
	65					70					75				80		
	Arg	Ser	Tyr	Ala	Asn	Gly	Asn	Trp	Ile	Tyr	Gly	Asp	Val	Leu	Cys	Ile	
					85					90					95		
15	Ser	Asn	Arg	Tyr	Val	Leu	His	Ala	Asn	Leu	Tyr	Thr	Ser	Ile	Leu	Phe	
				100					105					110			
	Leu	Thr	Phe	Ile	Ser	Ile	Asp	Arg	Tyr	Leu	Ile	Ile	Lys	Tyr	Pro	Phe	
			115					120					125				
	Arg	Glu	His	Leu	Leu	Gln	Lys	Lys	Glu	Phe	Ala	Ile	Leu	Ile	Ser	Leu	
		130					135					140					
20	Ala	Ile	Trp	Val	Leu	Val	Thr	Leu	Glu	Leu	Leu	Pro	Ile	Leu	Pro	Leu	
	145					150					155				160		
	Ile	Asn	Pro	Val	Ile	Thr	Asp	Asn	Gly	Thr	Thr	Cys	Asn	Asp	Phe	Ala	
				165						170					175		
25	Ser	Ser	Gly	Asp	Pro	Asn	Tyr	Asn	Leu	Ile	Tyr	Ser	Met	Cys	Leu	Thr	
				180					185					190			
	Leu	Leu	Gly	Phe	Leu	Ile	Pro	Leu	Phe	Val	Met	Cys	Phe	Phe	Tyr	Tyr	
			195					200					205				
	Lys	Ile	Ala	Leu	Phe	Leu	Lys	Gln	Arg	Asn	Arg	Gln	Val	Ala	Thr	Ala	
		210					215					220					
30	Leu	Pro	Leu	Glu	Lys	Pro	Leu	Asn	Leu	Val	Ile	Met	Ala	Val	Val	Ile	
	225					230					235				240		
	Phe	Ser	Val	Leu	Phe	Thr	Pro	Tyr	His	Val	Met	Arg	Asn	Val	Arg	Ile	
				245						250				255			
35	Ala	Ser	Arg	Leu	Gly	Ser	Trp	Lys	Gln	Tyr	Gln	Cys	Thr	Gln	Val	Val	
				260					265					270			
	Ile	Asn	Ser	Phe	Tyr	Ile	Val	Thr	Arg	Pro	Leu	Ala	Phe	Leu	Asn	Ser	

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	275		280		285
	Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp				
	290		295		300
5	Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe				
	305		310		315 320
	Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys				
		325		330	

(40) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

	ATGCAGGCGC TTAACATTAC CCCGGAGCAG TTCTCTCGGC TGCTGCGGGA CCACAACCTG	60
	ACGCGGGAGC AGTTCATCGC TCTGTACCGG CTGCGACCGC TCGTCTACAC CCCAGAGCTG	120
	CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC	180
	TTTGGCAATG CTCTGGTGTT CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC	240
20	AACATCTTTA TCTGCTCCTT GGCGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC	300
	GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGGG GTGCTTTCAT TTGCAAGATG	360
	GTGCCATTTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT	420
	GTGGAAGGC ACCAGGGACT TGTGCATCCT TTTAAAATGA AGTGGCAATA CACCAACCGA	480
	AGGGCTTTCA CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG	540
25	TGGCACGTGC AACAACTTGA GATCAAATAT GACTTCCTAT ATGAAAAGGA ACACATCTGC	600
	TGCTTAGAAG AGTGGACCAG CCCTGTGCAC CAGAAGATCT ACACCACCTT CATCCTTGTC	660
	ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAAT TGGTTATGAA	720
	CTTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCCTC GAACTATTCA TGGAAAAGAA	780
	ATGTCCAAAA TAGCCAGGAA GAAGAAACGA GCTGTCATTA TGATGGTGAC AGTGGTGGCT	840
30	CTCTTTGCTG TGTGCTGGGC ACCATTCCAT GTTGTCCATA TGATGATTGA ATACAGTAAT	900
	TTTGAAAAGG AATATGATGA TGTCACAATC AAGATGATTT TTGCTATCGT GCAAATTATT	960

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GGATTTTCCA ACTCCATCTG TAATCCCATT GTCTATGCAT TTATGAATGA AAACCTTCAA 1020
 AAAAATGTTT TGTCTGCAGT TTGTTATTGC ATAGTAAATA AAACCTTCTC TCCAGCACAA 1080
 AGGCATGGAA ATTCAGGAAT TACAATGATG CGGAAGAAAG CAAAGTTTTC CCTCAGAGAG 1140
 AATCCAGTGG AGGAAACCAA AGGAGAAGCA TTCAGTGATG GCAACATTGA AGTCAAATTG 1200
 5 TGTGAACAGA CAGAGGAGAA GAAAAAGCTC AAACGACATC TTGCTCTCTT TAGGTCTGAA 1260
 CTGGCTGAGA ATTCTCCTTT AGACAGTGGG CATTAA 1296

(41) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

15

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
 1 5 10 15

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
 20 25 30

20

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
 35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
 50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
 65 70 75 80

25

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
 85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
 100 105 110

30

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
 115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
 130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
 145 150 155 160

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	Arg	Ala	Phe	Thr	Met	Leu	Gly	Val	Val	Trp	Leu	Val	Ala	Val	Ile	Val	
						165					170				175		
	Gly	Ser	Pro	Met	Trp	His	Val	Gln	Gln	Leu	Glu	Ile	Lys	Tyr	Asp	Phe	
				180					185					190			
5	Leu	Tyr	Glu	Lys	Glu	His	Ile	Cys	Cys	Leu	Glu	Glu	Trp	Thr	Ser	Pro	
			195					200					205				
	Val	His	Gln	Lys	Ile	Tyr	Thr	Thr	Phe	Ile	Leu	Val	Ile	Leu	Phe	Leu	
		210					215					220					
10	Leu	Pro	Leu	Met	Val	Met	Leu	Ile	Leu	Tyr	Ser	Lys	Ile	Gly	Tyr	Glu	
	225					230					235					240	
	Leu	Trp	Ile	Lys	Lys	Arg	Val	Gly	Asp	Gly	Ser	Val	Leu	Arg	Thr	Ile	
				245					250						255		
	His	Gly	Lys	Glu	Met	Ser	Lys	Ile	Ala	Arg	Lys	Lys	Lys	Arg	Ala	Val	
			260						265					270			
15	Ile	Met	Met	Val	Thr	Val	Val	Ala	Leu	Phe	Ala	Val	Cys	Trp	Ala	Pro	
		275						280					285				
	Phe	His	Val	Val	His	Met	Met	Ile	Glu	Tyr	Ser	Asn	Phe	Glu	Lys	Glu	
		290					295					300					
20	Tyr	Asp	Asp	Val	Thr	Ile	Lys	Met	Ile	Phe	Ala	Ile	Val	Gln	Ile	Ile	
	305				310						315				320		
	Gly	Phe	Ser	Asn	Ser	Ile	Cys	Asn	Pro	Ile	Val	Tyr	Ala	Phe	Met	Asn	
				325					330						335		
	Glu	Asn	Phe	Lys	Lys	Asn	Val	Leu	Ser	Ala	Val	Cys	Tyr	Cys	Ile	Val	
			340					345					350				
25	Asn	Lys	Thr	Phe	Ser	Pro	Ala	Gln	Arg	His	Gly	Asn	Ser	Gly	Ile	Thr	
		355						360					365				
	Met	Met	Arg	Lys	Lys	Ala	Lys	Phe	Ser	Leu	Arg	Glu	Asn	Pro	Val	Glu	
		370					375					380					
30	Glu	Thr	Lys	Gly	Glu	Ala	Phe	Ser	Asp	Gly	Asn	Ile	Glu	Val	Lys	Leu	
	385				390					395						400	
	Cys	Glu	Gln	Thr	Glu	Glu	Lys	Lys	Lys	Leu	Lys	Arg	His	Leu	Ala	Leu	
				405						410					415		
	Phe	Arg	Ser	Glu	Leu	Ala	Glu	Asn	Ser	Pro	Leu	Asp	Ser	Gly	His		
			420					425						430			

35 (42) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGTGTACAG CAGTTCGCAG AGTG

24

(43) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

15 GAGTGCCAGG CAGAGCAGGT AGAC

24

(44) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- 20 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

25 CCCGAATTCC TGCTTGCTCC CAGCTTGCCC C

31

(45) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- 30 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTGGATCCT GCTGTCAAAG GTCCCATTCG GG

32

(46) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCACAATGCT AGGTGTGGTC

20

(47) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGCATAGACA ATGGGATTAC AG

22

(48) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCACAATGCT AGGTGTGGTC TGGCTGGTGG CAGTCATCGT AGGATCACCC ATGTGGCACC

60

TGCAACAAC TGAGATCAAA TATGACTTCC TATATGAAAA GGAACACATC TGCTGCTTAG

120

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AAGAGTGGAC CAGCCCTGTG CACCAGAAGA TCTACACCAC CTCATCCTT GTCATCCTCT 180
TCCTCCTGCC TCTTATGGTG ATGCTTATTC TGTACGTAAA ATTGGTTATG AACTTTGGAT 240
AAAGAAAAGA GTTGGGGATG GTTCAGTGCT TCGAACTATT CATGGAAAAG AAATGTCCAA 300
AATAGCCAGG AAGAAGAAAC GAGCTGTCAT TATGATGGTG ACAGTGGTGG CTCTCTTTGC 360
5 TGTGTGCTGG GCACCATTC ATGTTGTCCA TATGATGATT GAATACAGTA ATTTTGAAAA 420
GGAATATGAT GATGTCACAA TCAAGATGAT TTTTGCTATC GTGCAAATTA TTGGATTTTC 480
CAACTCCATC TGTAATCCCA TTGTCTATGC A 511

(49) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGCTTAGAA GAGTGGACCA G 21

(50) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGTGCACCA GAAGATCTAC AC 22

(51) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAAGGATGAA GGTGGTGTAG A

21

5 (52) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGTAGATCT TCTGGTGCAC AGG

23

15 (53) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCAATGCAGG TCATAGTGAG C

21

(54) INFORMATION FOR SEQ ID NO:53:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGGAGCATGG TGACGGGAAT GCAGAAG

27

(55) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTGATGAGCA GGTCCTGAG CGCCAAG

27

(56) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCAATGCAGG CGCTTAACAT TAC

23

(57) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 30 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTGGGTTACA ATCTGAAGGG CA

22

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(58) INFORMATION FOR SEQ ID NO:57:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

10 ACTCCGTGTC CAGCAGGACT CTG

23

(58) INFORMATION FOR SEQ ID NO:58:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

20 TGGCGTGTTC TGGACCCTCA CGTG

24

(58) INFORMATION FOR SEQ ID NO:59:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

30 CAGGCCTTGG ATTTTAATGT CAGGGATGG

29

(61) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGAGAGTCAG CTCTGAAAGA ATTCAGG

27

(62) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGATGTGATG CCAGATACTA ATAGCAC

27

(63) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCTGATTCAT TTAGGTGAGA TTGAGAC

27

(64) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(3) INFORMATION FOR SEQ ID NO:63:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTGGATCCA CATAATGCAT TTTCTC

26

(66) INFORMATION FOR SEQ ID NO:65:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCCAAA 60
GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCTACTT TATACAGTAT CATCTTTGTG 120
GTGGGAATAT TTGGAAACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG 180
ACTGTGGCCA GTGTTTTTCT TTTGAATTTA GCACTGGCTG ACTTATGCTT TTTACTGACT 240
25 TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTTGG CAATTACCTA 300
TGTAAGATTG CTTAGCCAG CGTCAGTTT AACCTGTACG CTAGTGTGTT TCTACTCACG 360
TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTACCCAA TGAAGTCCCG CCTTCGACGC 420
ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTTGGC TGCTGGCAGG CTTGGCCAGT 480
TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTTGT 540
30 GCTTTCCATT ATGAGTCCCA AAATTCAACC CTCCGATAG GGCTGGGCCT GACCAAAAAT 600

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ATACTGGGTT TCCTGTTTCC TTTTCTGATC ATTCTTACAA GTTATACTCT TATTTGGAAG 660
 GCCCTAAAGA AGGCTTATGA AATTCAGAAG AACAAACCAA GAAATGATGA TATTTTAAAG 720
 ATAATTATGG CAATTGTGCT TTTCTTTTTC TTTTCCTGGA TTCCCCACCA AATATTCACT 780
 TTTCTGGATG TATTGATTCA ACTAGGCATC ATACGTGACT GTAGAATTGC AGATATTGTG 840
 5 GACACGGCCA TGCCTATCAC CATTGTGATA GCTTATTTTA ACAATTGCCT GAATCCTCTT 900
 TTTTATGGCT TTCTGGGGAA AAAATTTAAA AGATATTTTC TCCAGCTTCT AAAATATATT 960
 CCCCCAAAAG CCAAATCCCA CTCAAACCTT TCAACAAAAA TGAGCACGCT TTCCTACCGC 1020
 CCCTCAGATA ATGTAAGCTC ATCCACCAAG AAGCCTGCAC CATGTTTGA GGTGAGTGA 1080

(67) INFORMATION FOR SEQ ID NO:66:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
 1 5 10 15
 Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
 20 20 25 30
 Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
 35 40 45
 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
 50 55 60
 25 Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
 65 70 75 80
 Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
 85 90 95
 30 Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
 100 105 110
 Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
 115 120 125
 Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val

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	130		135		140
	Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser				
	145		150		155 160
5	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn				
		165		170	175
	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro				
		180		185	190
	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe				
		195		200	205
10	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys				
		210		215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys				
		225		230	235 240
15	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His				
		245		250	255
	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg				
		260		265	270
	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile				
		275		280	285
20	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe				
		290		295	300
	Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile				
		305		310	315 320
25	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr				
		325		330	335
	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro				
		340		345	350
	Ala Pro Cys Phe Glu Val Glu				
		355			

30 (68) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACCATGGGCA GCCCCTGGAA CGGCAGC

27

(69) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGAACCACCA CCAGCAGGAC GCGGACGGTC TGCCGGTGG

39

(70) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

20 GTCCGCGTCC TGCTGGTGGT GGTCTGGCA TTTATAATT

39

(71) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CCTGGATCCT TATCCCATCG TCTTCACGTT AGC

33

30 (72) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

5 CTGGAATTCT CCTGCCAGCA TGGTGA
26

(73) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCAGGATCCT ATATTGCGTG CTCTGTCCCC
30

(74) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATGGTGA ACT CCACCCACCG TGGGATGCAC ACTTCTCTGC ACCTCTGGAA CCGCAGCAGT 60
TACAGACTGC ACAGCAATGC CAGTGAGTCC CTTGGAAAAG GCTACTCTGA TGGAGGGTGC 120
TACGAGCAAC TTTTGTCTC TCCTGAGGTG TTTGTGACTC TGGGTGTCAT CAGCTTGTG 180
GAGAATATCT TAGTGATTGT GGCAATAGCC AAGAACAAGA ATCTGCATTC ACCCATGTAC 240
30 TTTTTCATCT GCAGCTTGGC TGTGGCTGAT ATGCTGGTGA GCGTTTCAAA TGGATCAGAA 300
ACCATTATCA TCACCCTATT AAACAGTACA GATACGGATG CACAGAGTTT CACAGTGAAT 360
ATTGATAATG TCATTGACTC GGTGATCTGT AGCTCCTTGC TTGCATCCAT TTGCAGCCTG 420

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CTTTCAATTG CAGTGGACAG GTACTTTACT ATCTTCTATG CTCTCCAGTA CCATAACATT 480
 ATGACAGTTA AGCGGGTTGG GATCAGCATA AGTTGTATCT GGGCAGCTTG CACGGTTTCA 540
 GGCATTTTGT TCATCATTTA CTCAGATAGT AGTGCTGTCA TCATCTGCCT CATCACCATG 600
 TTCTTCACCA TGCTGGCTCT CATGGCTTCT CTCTATGTCC ACATGTTCTT GATGGCCAGG 660
 5 CTTACACATTA AGAGGATTGC TGTCTCCCC GGCACCTGGT CCATCCGCCA AGGTGCCAAT 720
 ATGAAGGGAG CGATTACCTT GACCATCCTG ATTGGCGTCT TTGTTGTCTG CTGGGCCCCA 780
 TTCTTCCTCC ACTTAATATT CTACATCTCT TGTCTCAGA ATCCATATTG TGTGTGCTTC 840
 ATGTCTCACT TTAACCTGTA TCTCATACTG ATCATGTGTA ATTCAATCAT CGATCCTCTG 900
 ATTTATGCAC TCCGGAGTCA AGAACTGAGG AAAACCTTCA AAGAGATCAT CTGTTGCTAT 960
 10 CCCCTGGGAG GCCTTTGTGA CTTGTCTAGC AGATATTAA 999

(75) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
 20 1 5 10 15
 Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly
 20 25 30
 Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro
 35 40 45
 25 Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu
 50 55 60
 Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr
 65 70 75 80
 Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser
 30 85 90 95
 Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr
 100 105 110
 Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val

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	115	120	125
	Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala		
	130	135	140
5	Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile		
	145	150	155 160
	Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala		
		165	170 175
	Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala		
		180	185 190
10	Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met		
		195	200 205
	Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys		
		210	215 220
15	Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn		
		225	230 235 240
	Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val		
		245	250 255
	Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro		
		260	265 270
20	Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu		
		275	280 285
	Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu		
		290	295 300
25	Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr		
		305	310 315 320
	Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr		
		325	330

(76) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCGAAGCTTC GAGCTGAGTA AGGCGGCGGG CT

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(77) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTGGAATTCA TTTGCCCTGC CTCAACCCCC A

31

10 (78) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATGGAGCTGC TAAAGCTGAA CCGGAGCGTG CAGGGAACCG GACCCGGGCC GGGGGCTTCC 60
CTGTGCCGCC CGGGGGCGCC TCTCCTCAAC AGCAGCAGTG TGGGCAACCT CAGCTGCGAG 120
20 CCCCCTCGCA TTCGCGGAGC CGGGACACGA GAATTGGAGC TGGCCATTAG AATCACTCTT 180
TACGCAGTGA TCTTCCTGAT GAGCGTTGGA GGAAATATGC TCATCATCGT GGTCTTGGGA 240
CTGAGCCGCC GCCTGAGGAC TGTCACCAAT GCCTTCCTCC TCTACTGGC AGTCAGCGAC 300
CTCCTGCTGG CTGTGGCTTG CATGCCCTTC ACCCTCCTGC CCAATCTCAT GGGCACATTC 360
ATCTTTGGCA CCGTCATCTG CAAGGCGGTT TCCTACCTCA TGGGGGTGTC TGTGAGTGTG 420
25 TCCACGCTAA GCCTCGTGGC CATCGCACTG GAGCGATATA GCGCCATCTG CCGACCACTG 480
CAGGCACGAG TGTGGCAGAC GCGCTCCAC GCGGCTCGCG TGATTGTAGC CACGTGGCTG 540
CTGTCCGGAC TACTCATGGT GCCCTACCCC GTGTACACTG TCGTGCAACC AGTGGGGCCT 600
CGTGTGCTGC AGTGCGTGCA TCGCTGCCCC AGTGCGCGGG TCCGCCAGAC CTGGTCCGTA 660
CTGCTGCTTC TGCTCTTGTT CTTTCATCCA GGTGTGGTTA TGGCCGTGGC CTACGGGCTT 720
30 ATCTCTCGCG AGCTCTACTT AGGGCTTCGC TTGACGGCG ACAGTGACAG CGACAGCCAA 780
AGCAGGGTCC GAAACCAAGG CGGGCTGCCA GGGGCTGTTC ACCAGAACGG GCGTTGCCGG 840

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CCTGAGACTG GCGCGGTTGG CAAAGACAGC GATGGCTGCT ACGTGCAACT TCCACGTTCC 900
 CGGCCTGCCC TGGAGCTGAC GCGCGTGACG GCTCCTGGGC CGGGATCCGG CTCCCAGCCC 960
 ACCCAGGCCA AGCTGCTGGC TAAGAAGCGC GTGGTGCGAA TGTTGCTGGT GATCGTTGTG 1020
 CTTTTTTTTT TGTGTTGGTT GCCAGTTTAT AGTGCCAACA CGTGGCGCGC CTTTGATGGC 1080
 5 CCGGGTGCAC ACCGAGCACT CTCGGGTGCT CCTATCTCCT TCATTCACTT GCTGAGCTAC 1140
 GCCTCGGCCT GTGTCAACCC CCTGGTCTAC TGCTTCATGC ACCGTCGCTT TCGCCAGGCC 1200
 TGCTTGAAA CTTGCGCTCG CTGCTGCCCC CGGCCTCCAC GAGCTCGCCC CAGGGCTCTT 1260
 CCCGATGAGG ACCCTCCAC TCCCTCCATT GCTTCGCTGT CCAGGCTTAG CTACACCACC 1320
 ATCAGCACAC TGGGCCCTGG CTGA 1344

10 (79) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

15 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
 1 5 10 15
 20 Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
 20 25 30
 Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
 35 40 45
 25 Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
 50 55 60
 Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
 65 70 75 80
 Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
 85 90 95
 30 Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu
 100 105 110
 Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys
 115 120 125

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	Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser	
	130	135 140
	Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu	
	145	150 155 160
5	Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val	
		165 170 175
	Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr	
		180 185 190
10	Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg	
		195 200 205
	Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu	
		210 215 220
	Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu	
		225 230 235 240
15	Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp	
		245 250 255
	Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala	
		260 265 270
20	Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys	
		275 280 285
	Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu	
		290 295 300
	Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro	
		305 310 315 320
25	Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Val Arg Met Leu Leu	
		325 330 335
	Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala	
		340 345 350
30	Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser	
		355 360 365
	Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys	
		370 375 380
	Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala	
		385 390 395 400
35	Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg	
		405 410 415
	Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser	

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420

425

430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
 435 440 445

(80) INFORMATION FOR SEQ ID NO:79:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TGCAAGCTTA AAAAGGAAAA AATGAACAGC

30

(81) INFORMATION FOR SEQ ID NO:80:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TAAGGATCCC TTCCCTTCAA AACATCCTTG

30

(82) INFORMATION FOR SEQ ID NO:81:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

30 ATGAACAGCA CATGTATTGA AGAACAGCAT GACCTGGATC ACTATTTGTT TCCCATTGTT 60
 TACATCTTTG TGATTATAGT CAGCATTCCA GCCAATATTG GATCTCTGTG TGTGTCTTTC 120
 CTGCAACCCA AGAAGGAAAG TGAAGTAGGA ATTTACCTCT TCAGTTTGTC ACTATCAGAT 180
 TTAATCTATG CATTAATCTT CCCTTTATGG ATTGATTATA CTTGGAATAA AGACAATG 240

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ACTTTCTCTC CTGCCCTTGTG CAAAGGGAGT GCTTTTCTCA TGTACATGAA GTTTTACAGC 300
 AGCACAGCAT TCCTCACCTG CATTGCCGTT GATCGGTATT TGGCTGTTGT CTACCCCTTG 360
 AAGTTTTTTT TCCTAAGGAC AAGAAGAATT GCACTCATGG TCAGCCTGTC CATCTGGATA 420
 TTGGAAACCA TCTTCAATGC TGTCAATGTT TGGGAAGATG AAACAGTTGT TGAATATTGC 480
 5 GATGCCGAAA AGTCTAATTT TACTTTATGC TATGACAAAT ACCCTTTAGA GAAATGGCAA 540
 ATCAACCTCA ACTTGTTTCTG GACGTGTACA GGCTATGCAA TACCTTTGGT CACCATCCTG 600
 ATCTGTAACC GGAAAGTCTA CCAAGCTGTG CGGCACAATA AAGCCACGGA AAACAAGGAA 660
 AAGAAGAGAA TCATAAAACT ACTTGTCAGC ATCAGAGTTA CTTTGTCTT ATGCTTTTACT 720
 CCCTTTCATG TGATGTTGCT GATTCGCTGC ATTTTAGAGC ATGCTGTGAA CTTCGAAGAC 780
 10 CACAGCAATT CTGGGAAGCG AACTTACACA ATGTATAGAA TCACGGTTGC ATTAACAAGT 840
 TTAAATTGTG TTGCTGATCC AATTCTGTAC TGTTTTGTGA CCGAAACAGG AAGATATGAT 900
 ATGTGGAATA TATTAAATTT CTGCACTGGG AGGTGTAATA CATCACAAAG ACAAAGAAAA 960
 CGCATACTTT CTGTGTCTAC AAAAGATACT ATGGAATTAG AGGTCCTTGA GTAG 1014

(83) INFORMATION FOR SEQ ID NO:82:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu
 1 5 10 15
 Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn
 25 20 25 30
 Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu
 35 40 45
 Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
 50 55 60
 30 Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
 65 70 75 80
 Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met

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	85	90	95
	Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg		
	100	105	110
5	Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg		
	115	120	125
	Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile		
	130	135	140
	Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys		
	145	150	155
10	Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu		
	165	170	175
	Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr		
	180	185	190
15	Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln		
	195	200	205
	Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile		
	210	215	220
	Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr		
	225	230	235
20	Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val		
	245	250	255
	Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr		
	260	265	270
25	Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile		
	275	280	285
	Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile		
	290	295	300
	Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys		
	305	310	315
30	Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu		
	325	330	335
	Glu		

(84) INFORMATION FOR SEQ ID NO:83:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

5 CAGGAAGAAG AAACGAGCTG TCATTATGAT GGTGACAGTG
40

(85) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

15 CACTGTCACC ATCATAATGA CAGCTCGTTT CTCCTTCCTG
40

(86) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

25 GGCCACCGGC AGACCAAACG CGTCCTGCTG
30

(87) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

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CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T
31

(88) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGAAAAGAAG AGAATCAAAA AACTACTTGT CAGCATC 37

(89) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

20 CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T 31

(90) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCCAAA 60

30 GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCCTACTT TATACAGTAT CATCTTTGTG 120

GTGGGAATAT TTGGAAACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG 180

ACTGTGGCCA GTGTTTTTCT TTTGAATTGA GCACTGGCTG ACTTATGCTT TTTACTGACT 240

TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTTGG CAATTACCTA 300

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TGTAAGATTG CTTCAGCCAG CGTCAGTTTC AACCTGTACG CTAGTGTGTT TCTACTCAG 360
 TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC 420
 ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGGC TGCTGGCAGG CTTGGCCAGT 480
 TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTTGT 540
 5 GCTTTCATT ATGAGTCCCA AAATCAACC CTTCCGATAG GGCTGGGCCT GACCAAAAAT 600
 ATACTGGGTT TCCTGTTTCC TTTTCTGATC ATTCTTACAA GTTATACTCT TATTGGAAG 660
 GCCCTAAAGA AGGCTTATGA AATTCAAGG AACAAACCAA GAAATGATGA TATTAAAAAG 720
 ATAATTATGG CAATTGTGCT TTTCTTTTTC TTTTCTGGA TTCCCCACCA AATATTCAT 780
 TTTCTGGATG TATTGATTCA ACTAGGCATC ATACGTGACT GTAGAATTGC AGATATTGTG 840
 10 GACACGGCCA TGCCTATCAC CATTGTATA GCTTATTTTA ACAATTGCCT GAATCCTCTT 900
 TTTTATGGCT TTCTGGGGAA AAAATTAAA AGATATTTTC TCCAGCTTCT AAAATATATT 960
 CCCCCAAAAG CCAAATCCCA CTCAACCTT TCAACAAAA TGAGCACGCT TTCCTACCGC 1020
 CCCTCAGATA ATGTAAGCTC ATCCACCAAG AAGCCTGCAC CATGTTTGA GGTGAGTGA 1080

(91) INFORMATION FOR SEQ ID NO:90:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

- 20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
 1 5 10 15
 Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
 25 20 25 30
 Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
 35 40 45
 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
 50 55 60
 30 Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
 65 70 75 80
 Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe

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	85	90	95
	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu		
	100	105	110
5	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155 160
10	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
	165	170	175
	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
15	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Lys Lys		
	225	230	235 240
20	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His		
	245	250	255
	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg		
	260	265	270
25	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile		
	275	280	285
	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe		
	290	295	300
	Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile		
	305	310	315 320
30	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr		
	325	330	335
	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro		
	340	345	350
35	Ala Pro Cys Phe Glu Val Glu		
	355		

(92) INFORMATION FOR SEQ ID NO:91:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:
- CCAAGAAATG ATGATATTAA AAAGATAATT ATGGC 35
- (93) INFORMATION FOR SEQ ID NO:92:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:
- CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T 31
- (94) INFORMATION FOR SEQ ID NO:93:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
- ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCCAAA 60
- GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCCTACTT TATACAGTAT CATCTTTGTG 120
- GTGGGAATAT TTGGAAACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG 180
- ACTGTGGCCA GTGTTTTTCT TTTGAATTGA GCACTGGCTG ACTTATGCTT TTTACTGACT 240
- TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTTGG CAATTACCTA 300
- TGTAAGATTG CTTAGCCAG CGTCAGTTTC GCCCTGTACG CTAGTGTGTT TCTACTCACG 360
- TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC 420

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ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGC TGCTGGCAGG CTTGGCCAGT 480
 TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTTGT 540
 GCTTTCCATT ATGAGTCCCA AAATTCAACC CTTCCGATAG GGCTGGGCCT GACCAAAAAT 600
 ATACTGGGTT TCCTGTTTCC TTTTCTGATC ATTCTTACAA GTTATACTCT TATTTGGAAG 660
 5 GCCCTAAAGA AGGCTTATGA AATTCAGAAG AACAAACCAA GAAATGATGA TATTTTTAAG 720
 ATAATTATGG CAATTGTGCT TTTCTTTTTC TTTTCTGGA TTCCCCACCA AATATTCACT 780
 TTTCTGGATG TATTGATTCA ACTAGGCATC ATACGTGACT GTAGAATTGC AGATATTGTG 840
 GACACGGCCA TGCCTATCAC CATTGTGATA GCTTATTTTA ACAATTGCCT GAATCCTCTT 900
 TTTTATGGCT TTCTGGGGAA AAAATTTAAA AGATATTTTC TCCAGCTTCT AAAATATATT 960
 10 CCCCCAAAAG CCAAATCCCA CTCAAACCTT TCAACAAAAA TGAGCACGCT TTCCTACCGC 1020
 CCCTCAGATA ATGTAAGCTC ATCCACCAAG AAGCCTGCAC CATGTTTGA GGTGAGTGA 1080

(95) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 15 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

20 Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
 1 5 10 15
 Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
 20 25 30
 25 Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
 35 40 45
 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
 50 55 60
 Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
 65 70 75 80
 30 Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
 85 90 95
 Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Ala Leu

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	100	105	110
	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
5	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155 160
	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
		165	170 175
10	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
		180	185 190
	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
		195	200 205
15	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
		210	215 220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys		
		225	230 235 240
	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His		
		245	250 255
20	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg		
		260	265 270
	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile		
		275	280 285
25	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe		
		290	295 300
	Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile		
		305	310 315 320
	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr		
		325	330 335
30	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro		
		340	345 350
	Ala Pro Cys Phe Glu Val Glu		
		355	

(97) INFORMATION FOR SEQ ID NO:95:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(97) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CCTGCAGGCG AAAGTGACTC TGGCTGAAG

29

(98) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTGTACGCTA GTGTGTTTCT ACTCAGTGT CTCAGCATTG AT

42

(99) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGATCCA CATAATGCAT TTTCTC

26

(100) INFORMATION FOR SEQ ID NO:99:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGATTCTCA	ACTCTTCTAC	TGAAGATGGT	ATTAAAAGAA	TCCAAGATGA	TTGTCCCAAA	60
GCTGGAAGGC	ATAATTACAT	ATTTGTCATG	ATTCCTACTT	TATACAGTAT	CATCTTTGTG	120
GTGGGAATAT	TTGGAAACAG	CTTGGTGGTG	ATAGTCATTT	ACTTTTATAT	GAAGCTGAAG	180
15 ACTGTGGCCA	GTGTTTTTCT	TTTGAATTTA	GCACTGGCTG	ACTTATGCTT	TTTACTGACT	240
TTGCCACTAT	GGGCTGTCTA	CACAGCTATG	GAATACCGCT	GGCCCTTTGG	CAATTACCTA	300
TGTAAGATTG	CTTCAGCCAG	CGTCAGTTTC	AACCTGTACG	CTAGTGTGTT	TCTACTCACG	360
TGTCTCAGCA	TTGATCGATA	CCTGGCTATT	GTTCAACCAA	TGAAGTCCCG	CCTTCGACGC	420
ACAATGCTTG	TAGCCAAAGT	CACCTGCATC	ATCATTTGGC	TGCTGGCAGG	CTTGGCCAGT	480
20 TTGCCAGCTA	TAATCCATCG	AAATGTATTT	TTCATTGAGA	ACACCAATAT	TACAGTTTGT	540
GCTTTCCATT	ATGAGTCCCA	AAATTCAACC	CTTCCGATAG	GGCTGGGCCT	GACCAAAAAT	600
ATACTGGGTT	TCCTGTTTCC	TTTTCTGATC	ATTCTTACAA	GTTATTTTGG	AATTCGAAAA	660
CACTTACTGA	AGACGAATAG	CTATGGGAAG	AACAGGATAA	CCCGTGACCA	AGTTAAGAAG	720
ATAATTATGG	CAATTGTGCT	TTTCTTTTTC	TTTTCTGGA	TTCCCCACCA	AATATTCACT	780
25 TTTCTGGATG	TATTGATTCA	ACTAGGCATC	ATACGTGACT	GTAGAATTGC	AGATATTGTG	840
GACACGGCCA	TGCCTATCAC	CATTTGTATA	GCTTATTTTA	ACAATTGCCT	GAATCCTCTT	900
TTTTATGGCT	TTCTGGGGAA	AAAATTAA	AGATATTTTC	TCCAGCTTCT	AAAATATATT	960
CCCCCAAAG	CCAAATCCCA	CTCAAACCTT	TCAACAAAA	TGAGCACGCT	TTCCTACCGC	1020
CCCTCAGATA	ATGTAAGCTC	ATCCACCAAG	AAGCCTGCAC	CATGTTTTGA	GTTGAGTGA	1080

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(101) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

10 Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
 1 5 10 15
 Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
 20 25 30
 Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
 35 40 45
 15 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
 50 55 60
 Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
 65 70 75 80
 20 Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
 85 90 95
 Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
 100 105 110
 Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
 115 120 125
 25 Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
 130 135 140
 Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
 145 150 155 160
 30 Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
 165 170 175
 Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
 180 185 190
 Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
 195 200 205
 35 Leu Ile Ile Leu Thr Ser Tyr Phe Gly Ile Arg Lys His Leu Leu Lys
 210 215 220

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Thr Asn Ser Tyr Gly Lys Asn Arg Ile Thr Arg Asp Gln Val Lys Lys
 225 230 235 240
 Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His
 245 250 255
 5 Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
 260 265 270
 Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
 275 280 285
 10 Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
 290 295 300
 Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
 305 310 315 320
 Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
 325 330 335
 15 Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
 340 345 350
 Ala Pro Cys Phe Glu Val Glu
 355

(102) INFORMATION FOR SEQ ID NO:101:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: DNA (genomic)
 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCCGAATTCC AAAATAACTT GTAAGAATGA TCAGAAA

37

(103) INFORMATION FOR SEQ ID NO:102:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: DNA (genomic)
 (iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AGATCTTAAG AAGATAATTA TGGCAATTGT GCT

33

(104) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AATTCGAAAA CACTTACTGA AGACGAATAG CTATGGGAAG AACAGGATAA CCCGTGACCA

60

AG

62

(105) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTAACTTGGT CACGGGTTAT CCTGTTCTTC CCATAGCTAT TCGTCTTCAG TAAGTGTTTT

60

CG

62

25 (106) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1083 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

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ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCCAAA   60
GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCCTACTT TATACAGTAT CATCTTTGTG   120
GTGGGAATAT TTGGAAACAG CTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG   180
ACTGTGGCCA GTGTTTTTCT TTTGAATTTA GCACTGGCTG ACTTATGCTT TTTACTGACT   240
5  TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTTGG CAATTACCTA   300
TGTAAGATTG CTTAGCCAG CGTCAGTTTC AACCTGTACG CTAGTGTGTT TCTACTCAGC   360
TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC   420
ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGC TGCTGGCAGG CTGGCCAGT   480
TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTTGT   540
10 GCTTTCCATT ATGAGTCCCA AAATTCAACC CTTCCGATAG GGCTGGGCCT GACCAAAAAT   600
ATACTGGGTT TCCTGTTTCC TTTTCTGATC ATTCTTACAA GTTATACTCT TATTTGGAAG   660
GCCCTAAAGA AGGCTTATGA AATTCAGAAG AACAAACCAA GAAATGATGA TATTTTAAAG   720
ATAATTATGG CAGCAATTGT GCTTTTCTTT TTCTTTTCTT GGATTCCCCA CCAATATTC   780
ACTTTTCTGG ATGTATTGAT TCAACTAGGC ATCATACGTG ACTGTAGAAT TGCAGATATT   840
15 GTGGACACGG CCATGCCTAT CACCATTGT ATAGCTTATT TTAACAATTG CCTGAATCCT   900
CTTTTTTATG GCTTCTGGG GAAAAAATTT AAAAGATATT TTCTCCAGCT TCTAAATAT   960
ATTCCCCCAA AAGCCAAATC CCACTCAAAC CTTTCAACAA AAATGAGCAC GCTTTCCTAC  1020
CGCCCCTCAG ATAATGTAAG CTCATCCACC AAGAAGCCTG CACCATGTTT TGAGGTTGAG  1080
TGA                                                                    1083

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20 (107) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - 25 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1           5           10           15

```

30 Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro

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	20	25	30
	Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu		
	35	40	45
5	Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser		
	50	55	60
	Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr		
	65	70	75 80
	Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe		
		85 90	95
10	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu		
	100	105	110
	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
15	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155 160
	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
		165 170	175
20	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
25	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys		
	225	230	235 240
	Ile Ile Met Ala Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro		
		245 250	255
30	His Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile		
	260	265	270
	Arg Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr		
	275	280	285
35	Ile Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly		
	290	295	300
	Phe Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr		
	305	310	315 320

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Ile Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser
 325 330 335

Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys
 340 345 350

5 Pro Ala Pro Cys Phe Glu Val Glu
 355 360

(108) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 10 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(109) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AAGCACAATT GCTGCATAAT TATCTTAAAA ATATCATC

38

(110) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AAGATAATTA TGGCAGCAAT TGTGCTTTTC TTTTCTTT

39

(111) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGGATCCA CATAATGCAT TTTCTC

26

(112) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGGAGCTGC TAAAGCTGAA CCGGAGCGTG CAGGGAACCG GACCCGGGCC GGGGGCTTCC 60
CTGTGCCGCC CGGGGGCGCC TCTCCTCAAC AGCAGCAGTG TGGGCAACCT CAGCTGCGAG 120
CCCCCTCGCA TTCGCGGAGC CGGGACACGA GAATTGGAGC TGGCCATTAG AATCACTCTT 180
TACGCACTGA TCTTCCTGAT GAGCGTTGGA GGAAATATGC TCATCATCGT GGTCTCTGGA 240
25 CTGAGCCGCC GCCTGAGGAC TGTACCAAT GCCTTCCTCC TCTCACTGGC AGTCAGCGAC 300
CTCCTGCTGG CTGTGGCTTG CATGCCCTTC ACCCTCCTGC CCAATCTCAT GGGCACATTC 360
ATCTTTGGCA CCGTCATCTG CAAGGCGGTT TCCTACCTCA TGGGGGTGTC TGTGAGTGTG 420
TCCACGCTAA GCCTCGTGGC CATCGCACTG GAGCGATATA GCGCCATCTG CCGACCACTG 480
CAGGCACGAG TGTGGCAGAC GCGCTCCAC GCGGCTCGCG TGATTGTAGC CACGTGGCTG 540
30 CTGTCCGGAC TACTCATGGT GCCCTACCCC GTGTACACTG TCGTGCAACC AGTGGGGCCT 600
CGTGTGCTGC AGTGCCTGCA TCGCTGGCCC AGTGC GCGGG TCCGCCAGAC CTGGTCCGTA 660

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CTGCTGCTTC TGCTCTTGTT CTTTCATCCCA GGTGTGGTTA TGGCCGTGGC CTACGGGCTT 720
 ATCTCTCGCG AGCTCTACTT AGGGCTTCGC TTTGACGGCG ACAGTGACAG CGACAGCCAA 780
 AGCAGGGTCC GAAACCAAGG CGGGCTGCCA GGGGCTGTTC ACCAGAACGG GCGTTGCCGG 840
 CCTGAGACTG GCGCGGTTGG CAAAGACAGC GATGGCTGCT ACGTGCAACT TCCACGTTCC 900
 5 CGGCCTGCCC TGGAGCTGAC GGCCTGACG GCTCCTGGGC CGGGATCCGG CTCCCGGCCC 960
 ACCCAGGCCA AGCTGCTGGC TAAGAAGCGC GTGAAACGAA TGTGCTGGT GATCGTTGTG 1020
 CTTTTTTTTC TGTGTTGGTT GCCAGTTTAT AGTGCCAACA CGTGGCGCGC CTTTGATGGC 1080
 CCGGGTGAC ACCGAGCACT CTCGGGTGCT CCTATCTCCT TCATTCACTT GCTGAGCTAC 1140
 GCCTCGGCCT GTGTCAACCC CCTGGTCTAC TGCTTCATGC ACCGTCGCTT TCGCCAGGCC 1200
 10 TGCCTGGAAA CTTGCGCTCG CTGCTGCCCC CGGCCTCCAC GAGCTCGCCC CAGGGCTCTT 1260
 CCCGATGAGG ACCCTCCAC TCCCTCCATT GCTTCGCTGT CCAGGCTTAG CTACACCACC 1320
 ATCAGCACAC TGGGCCCTGG CTGA 1344

(113) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 447 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
 1 5 10 15
 Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
 20 25 30
 25 Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
 35 40 45
 Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
 50 55 60
 30 Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
 65 70 75 80
 Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
 85 90 95

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	Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu	
	100	105 110
	Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys	
	115	120 125
5	Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser	
	130	135 140
	Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu	
	145	150 155 160
10	Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val	
	165	170 175
	Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr	
	180	185 190
	Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg	
	195	200 205
15	Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu	
	210	215 220
	Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu	
	225	230 235 240
20	Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp	
	245	250 255
	Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala	
	260	265 270
	Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys	
	275	280 285
25	Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu	
	290	295 300
	Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro	
	305	310 315 320
30	Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu	
	325	330 335
	Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala	
	340	345 350
	Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser	
	355	360 365
35	Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys	
	370	375 380
	Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala	

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	385		390		395		400									
	Cys	Leu	Glu	Thr	Cys	Ala	Arg	Cys	Cys	Pro	Arg	Pro	Pro	Arg	Ala	Arg
					405					410					415	
5	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Asp	Pro	Pro	Thr	Pro	Ser	Ile	Ala	Ser
				420					425					430		
	Leu	Ser	Arg	Leu	Ser	Tyr	Thr	Thr	Ile	Ser	Thr	Leu	Gly	Pro	Gly	
				435				440					445			

(114) INFORMATION FOR SEQ ID NO:113:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CAGCAGCATG CGCTTCACGC GCTTCTTAGC CCAG

34

(115) INFORMATION FOR SEQ ID NO:114:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

25 AGAAGCGCGT GAAGCGCATG CTGCTGGTGA TCGTT

35

(116) INFORMATION FOR SEQ ID NO:115:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

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ATGGAGAAAA GAATCAAAAG AATGTTCTAT ATA

33

(117) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TATATAGAAC ATTCTTTTGA TTCTTTTCTC CAT

33

(118) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGCTCTCTGG CCTTGAAGCG CACGCTCAGC

30

(119) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCTGAGCGTG CGCTTCAAGG CCAGAGAGCG

30

(120) INFORMATION FOR SEQ ID NO:119:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCCAGGAAAA AGGTGAAAGT CAAAGTTTTC

30

10 (121) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAAAACTTTG ACTTTCACCT TTTTCCTGGG

30

20 (122) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGGGCGCGGG TGAAACGGCT GGTGAGC

27

30 (123) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

5 GCTCACCAGC CGTTTCACCC GCGCCCC

27

(124) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

15 CCCCTTGAAA AGCCTAAGAA CTTGGTCATC

30

(125) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

25 GATGACCAAG TTCTTAGGCT TTTCAAGGGG

30

(126) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GATCTCTAGA ATGAACAGCA CATGTATTGA AG

32

(127) INFORMATION FOR SEQ ID NO:126:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTAGGGTACC CGCTCAAGGA CCTCTAATTC CATAG

35

(128) INFORMATION FOR SEQ ID NO:127:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATGCAGGCGC TTAACATTAC CCCGGAGCAG TTCTCTCGGC TGCTGCGGGA CCACAACCTG	60
ACGCGGGAGC AGTTCATCGC TCTGTACCGG CTGCGACCGC TCGTCTACAC CCCAGAGCTG	120
CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC	180
25 TTTGGCAATG CTCTGGTGTT CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC	240
AACATCTTTA TCTGCTCCTT GCGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC	300
GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGGG GTGCTTTCAT TTGCAAGATG	360
GTGCCATTTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT	420
GTGGAAAGGC ACCAGGGACT TGTGCATCCT TTTAAAATGA AGTGGCAATA CACCAACCGA	480

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AGGGCTTTCA CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG 540
 TGGCACGTGC AACAACTTGA GATCAAATAT GACTTCCTAT ATGAAAAGGA ACACATCTGC 600
 TGCTTAGAAG AGTGGACCAG CCCTGTGCAC CAGAAGATCT ACACCACCTT CATCCTTGTC 660
 ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAAT TGGTTATGAA 720
 5 CTTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCTTC GAACTATTCA TGGAAAAGAA 780
 ATGTCCAAAA TAGCCAGGAA GAAGAAACGA GCTAAGATTA TGATGGTGAC AGTGGTGGCT 840
 CTCCTTGCTG TGTGCTGGGC ACCATTCCAT GTTGTCCATA TGATGATTGA ATACAGTAAT 900
 TTTGAAAAGG AATATGATGA TGTACAATC AAGATGATTT TTGCTATCGT GCAAATTATT 960
 GGATTTTCCA ACTCCATCTG TAATCCCATT GTCTATGCAT TTATGAATGA AAACCTTCAA 1020
 10 AAAAATGTTT TGTCTGCAGT TTGTTATTGC ATAGTAAATA AAACCTTCTC TCCAGCACAA 1080
 AGGCATGGAA ATTCAGGAAT TACAATGATG CGGAAGAAAG CAAAGTTTTC CCTCAGAGAG 1140
 AATCCAGTGG AGGAAACCAA AGGAGAAGCA TTCAGTGATG GCAACATTGA AGTCAAATTG 1200
 TGTGAACAGA CAGAGGAGAA GAAAAGCTC AAACGACATC TTGCTCTCTT TAGGTCTGAA 1260
 CTGGCTGAGA ATTCTCCTTT AGACAGTGGG CATTA 1296

15 (129) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

20 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
 1 5 10 15
 25 Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
 20 25 30
 Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
 35 40 45
 30 Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
 50 55 60
 Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
 65 70 75 80

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	Asn	Ile	Phe	Ile	Cys	Ser	Leu	Ala	Leu	Ser	Asp	Leu	Leu	Ile	Thr	Phe	85	90	95	
	Phe	Cys	Ile	Pro	Val	Thr	Met	Leu	Gln	Asn	Ile	Ser	Asp	Asn	Trp	Leu	100	105	110	
5	Gly	Gly	Ala	Phe	Ile	Cys	Lys	Met	Val	Pro	Phe	Val	Gln	Ser	Thr	Ala	115	120	125	
	Val	Val	Thr	Glu	Met	Leu	Thr	Met	Thr	Cys	Ile	Ala	Val	Glu	Arg	His	130	135	140	
10	Gln	Gly	Leu	Val	His	Pro	Phe	Lys	Met	Lys	Trp	Gln	Tyr	Thr	Asn	Arg	145	150	155	160
	Arg	Ala	Phe	Thr	Met	Leu	Gly	Val	Val	Trp	Leu	Val	Ala	Val	Ile	Val	165	170	175	
	Gly	Ser	Pro	Met	Trp	His	Val	Gln	Gln	Leu	Glu	Ile	Lys	Tyr	Asp	Phe	180	185	190	
15	Leu	Tyr	Glu	Lys	Glu	His	Ile	Cys	Cys	Leu	Glu	Glu	Trp	Thr	Ser	Pro	195	200	205	
	Val	His	Gln	Lys	Ile	Tyr	Thr	Thr	Phe	Ile	Leu	Val	Ile	Leu	Phe	Leu	210	215	220	
20	Leu	Pro	Leu	Met	Val	Met	Leu	Ile	Leu	Tyr	Ser	Lys	Ile	Gly	Tyr	Glu	225	230	235	240
	Leu	Trp	Ile	Lys	Lys	Arg	Val	Gly	Asp	Gly	Ser	Val	Leu	Arg	Thr	Ile	245	250	255	
	His	Gly	Lys	Glu	Met	Ser	Lys	Ile	Ala	Arg	Lys	Lys	Lys	Arg	Ala	Lys	260	265	270	
25	Ile	Met	Met	Val	Thr	Val	Val	Ala	Leu	Phe	Ala	Val	Cys	Trp	Ala	Pro	275	280	285	
	Phe	His	Val	Val	His	Met	Met	Ile	Glu	Tyr	Ser	Asn	Phe	Glu	Lys	Glu	290	295	300	
30	Tyr	Asp	Asp	Val	Thr	Ile	Lys	Met	Ile	Phe	Ala	Ile	Val	Gln	Ile	Ile	305	310	315	320
	Gly	Phe	Ser	Asn	Ser	Ile	Cys	Asn	Pro	Ile	Val	Tyr	Ala	Phe	Met	Asn	325	330	335	
	Glu	Asn	Phe	Lys	Lys	Asn	Val	Leu	Ser	Ala	Val	Cys	Tyr	Cys	Ile	Val	340	345	350	
35	Asn	Lys	Thr	Phe	Ser	Pro	Ala	Gln	Arg	His	Gly	Asn	Ser	Gly	Ile	Thr	355	360	365	
	Met	Met	Arg	Lys	Lys	Ala	Lys	Phe	Ser	Leu	Arg	Glu	Asn	Pro	Val	Glu				

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	370		375		380
	Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu				
	385		390		395 400
5	Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu				
		405		410	415
	Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His				
		420	425		430

(130) INFORMATION FOR SEQ ID NO:129:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2040 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGGGCAGCC CCTGGAACGG CAGCGACGGC CCCGAGGGGG CGCGGGAGCC GCCGTGGCCC
60

GCGCTGCCGC CTTGCGACGA GCGCCGCTGC TCGCCCTTTC CCCTGGGGGC GCTGGTGCCG
120

20 GTGACCGCTG TGTGCCTGTG CTTGTTCTG GTCGGGGTGA GCGGCAACGT GGTGACCGTG
180

ATGCTGATCG GCGCTACCG GGACATGCGG ACCACCACCA ACTTGTACCT GGGCAGCATG
240

25 GCCGTGTCCG ACCTACTCAT CTTGCTCGGG CTGCCGTTCTG ACCTGTACCG CCTCTGGCGC
300

TCGCGGCCCT GGTGTTTCGG GCCGCTGCTC TGCCGCCTGT CCTCTACGT GGGCGAGGGC
360

30 TGCACCTACG CCACGCTGCT GCACATGACC GCGCTCAGCG TCGAGCGCTA CCTGGCCATC
420

TGCCGCCCGC TCCGCGCCCG CGTCTTGGTC ACCCGGCGCC GCGTCCGCGC GTCATCGCT
480

35 GTGCTCTGGG CCGTGGCGCT GCTCTCTGCC GGTCCCTTCT TGTTCCTGGT GGGCGTCGAG
540

CAGGACCCCG GCATCTCCGT AGTCCCGGGC CTCATGGCA CCGCGCGGAT CGCCTCCTCG
600

40 CCTCTCGCCT CGTCGCCGCC TCTCTGGCTC TCGCGGGCGC CACCGCCGTC CCCGCCGTCTG

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660
GGGCCCCGAGA CCGCGGAGGC CGCGGCGCTG TTCAGCCGCG AATGCCGGCC GAGCCCCGCG
720
5 CAGCTGGGCG CGCTGCGTGT CATGCTGTGG GTCACCACCG CCTACTTCTT CCTGCCCTTT
780
CTGTGCCTCA GCATCCTCTA CGGGCTCATC GGGCGGGAGC TGTGGAGCAG CCGGCGGCCG
10 840
CTGCGAGGCC CGGCCGCCTC GGGGCGGGAG AGAGGCCACC GGCAGACCAA ACGCGTCCTG
900
15 CGTAAGTGGA GCCGCCGTGG TTCCAAAGAC GCCTGCCTGC AGTCCGCCCC GCCGGGGACC
960
GCGCAAACGC TGGGTCCCCT TCCCCTGCTC GCCCAGCTCT GGGCGCCGCT TCCAGCTCCC
1020
20 TTTCCTATTT CGATTCCAGC CTCCACCCGC CGGTACTTCC CATCCCCGA GAAAACCATG
1080
TCCTGTCCCC CAGGAGCTCT GGGGGACCCC AGGGCGCTTT GAGGGTGGGA TCCCCGATC
25 1140
CGATTAGTA ACCAGCAGTG CTTTTCCAGA GCCTCTGAGA CCAGAAAGGA GAGTTGGTAA
1200
30 TTCTTAATCC AACACCTGT TAGATGCCAC AATGAGGAG TCCTCACAGT GCTCTTGAGA
1260
AGACGAGGGA GATTTCAATTA AGCTAAAATT TTTTATTTAA TGTTAAGTGA TGCTGAAGGC
1320
35 TAAAGTAAAC CTGCTCGTA TCAAAAAGTA AAGATTGTGC AGACCTGTTG TAGAATTCCT
1380
TTCAACAGAG AACAGAAAAC TTGTCTCCGA AGTGGGTTTG TGGAAGGAAG CCTGCCAAGG
40 1440
CGGCTTGTTT AGAGAAATTG CTCCTTCTGG TTTATGTCCA GCCTTGATAA CACATATGGG
1500
45 AGCCTACTAT GCAGTTTTAA AGCAAGTATC CATGCAGCCT GCAGCCTGGT CATTTTTTCT
1560
GGGGTGAGGA TCTGCCTAGG TAGAAGTTTT CTCTAATTTA TTTTGCTGTT ACTTGTTATT
1620
50 GCAGATGGTT CCTGTGCGG GTGGGGGGTT TATTGCTTC CCAATGCTT TGTTAATCCC
1680
GGTGTGTGT CTTATGTTGC AGTGGTGGTG GTTCTGGCAT TTATAATTG CTGGTTGCCC
55 1740

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TTCCACGTTG GCAGAATCAT TTACATAAAC ACGGAAGATT CGCGGATGAT GTACTTCTCT
 1800

5 CAGTACTTTA ACATCGTCGC TCTGCAACTT TTCTATCTGA GCGCATCTAT CAACCCAATC
 1860

CTCTACAACC TCATTTCAAA GAAGTACAGA GCGGCGGCCT TTAACTGCT GCTCGCAAGG
 1920

10 AAGTCCAGGC CGAGAGGCTT CCACAGAAGC AGGGACACTG CGGGGGAAGT TGCAGGGGAC
 1980

ACTGGAGGAG ACACGGTGGG CTACACCGAG ACAAGCGCTA ACGTGAAGAC GATGGGATAA
 15 2040

(131) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

25 Met Gly Ser Pro Trp Asn Gly Ser Asp Gly Pro Glu Gly Ala Arg Glu
 1 5 10 15

Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro
 20 25 30

Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu
 35 40 45

30 Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly
 50 55 60

Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met
 65 70 75 80

35 Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr
 85 90 95

Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg
 100 105 110

Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His
 115 120 125

40 Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu
 130 135 140

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	Arg	Ala	Arg	Val	Leu	Val	Thr	Arg	Arg	Arg	Val	Arg	Ala	Leu	Ile	Ala	145	150	155	160
	Val	Leu	Trp	Ala	Val	Ala	Leu	Leu	Ser	Ala	Gly	Pro	Phe	Leu	Phe	Leu	165	170	175	
5	Val	Gly	Val	Glu	Gln	Asp	Pro	Gly	Ile	Ser	Val	Val	Pro	Gly	Leu	Asn	180	185	190	
	Gly	Thr	Ala	Arg	Ile	Ala	Ser	Ser	Pro	Leu	Ala	Ser	Ser	Pro	Pro	Leu	195	200	205	
10	Trp	Leu	Ser	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Pro	Ser	Gly	Pro	Glu	Thr	210	215	220	
	Ala	Glu	Ala	Ala	Ala	Leu	Phe	Ser	Arg	Glu	Cys	Arg	Pro	Ser	Pro	Ala	225	230	235	240
	Gln	Leu	Gly	Ala	Leu	Arg	Val	Met	Leu	Trp	Val	Thr	Thr	Ala	Tyr	Phe	245	250	255	
15	Phe	Leu	Pro	Phe	Leu	Cys	Leu	Ser	Ile	Leu	Tyr	Gly	Leu	Ile	Gly	Arg	260	265	270	
	Glu	Leu	Trp	Ser	Ser	Arg	Arg	Pro	Leu	Arg	Gly	Pro	Ala	Ala	Ser	Gly	275	280	285	
20	Arg	Glu	Arg	Gly	His	Arg	Gln	Thr	Lys	Arg	Val	Leu	Leu	Val	Val	Val	290	295	300	
	Leu	Ala	Phe	Ile	Ile	Cys	Trp	Leu	Pro	Phe	His	Val	Gly	Arg	Ile	Ile	305	310	315	320
	Tyr	Ile	Asn	Thr	Glu	Asp	Ser	Arg	Met	Met	Tyr	Phe	Ser	Gln	Tyr	Phe	325	330	335	
25	Asn	Ile	Val	Ala	Leu	Gln	Leu	Phe	Tyr	Leu	Ser	Ala	Ser	Ile	Asn	Pro	340	345	350	
	Ile	Leu	Tyr	Asn	Leu	Ile	Ser	Lys	Lys	Tyr	Arg	Ala	Ala	Ala	Phe	Lys	355	360	365	
30	Leu	Leu	Leu	Ala	Arg	Lys	Ser	Arg	Pro	Arg	Gly	Phe	His	Arg	Ser	Arg	370	375	380	
	Asp	Thr	Ala	Gly	Glu	Val	Ala	Gly	Asp	Thr	Gly	Gly	Asp	Thr	Val	Gly	385	390	395	400
	Tyr	Thr	Glu	Thr	Ser	Ala	Asn	Val	Lys	Thr	Met	Gly					405	410		

35 (132) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1344 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGGAGCTGC TAAAGCTGAA CCGGAGCGTG CAGGGAACCG GACCCGGGCC GGGGGCTTCC
60

CTGTGCCGCC CGGGGGCGCC TCTCCTCAAC AGCAGCAGTG TGGGCAACCT CAGCTGCGAG
120

10 CCCCCTCGCA TTCGCGGAGC CGGGACACGA GAATTGGAGC TGGCCATTAG AATCACTCTT
180

TACGCAGTGA TCTTCCTGAT GAGCGTTGGA GGAAATATGC TCATCATCGT GGTCTTGGA
240

15 CTGAGCCGCC GCCTGAGGAC TGTACCAAT GCCTTCCTCC TCTCACTGGC AGTCAGCGAC
300

CTCCTGCTGG CTGTGGCTTG CATGCCCTTC ACCCTCCTGC CCAATCTCAT GGGCACATTC
360

ATCTTTGGCA CCGTCATCTG CAAGGCGGTT TCCTACCTCA TGGGGGTGTC TGTGAGTGTG
420

20 TCCACGCTAA GCCTCGTGGC CATCGCACTG GAGCGATATA GCGCCATCTG CCGACCACTG
480

CAGGCACGAG TGTGGCAGAC GCGCTCCAC GCGGCTCGCG TGATTGTAGC CACGTGGCTG
540

25 CTGTCCGGAC TACTCATGGT GCCCTACCCC GTGTACACTG TCGTGCAACC AGTGGGGCCT
600

CGTGTGCTGC AGTGCGTGCA TCGCTGGCCC AGTGCGCGGG TCCGCCAGAC CTGGTCCGTA
660

CTGCTGCTTC TGCTCTTGTT CTTATCCCA GGTGTGGTTA TGGCCGTGGC CTACGGGCTT
720

30 ATCTCTCGCG AGCTCTACTT AGGGCTTCGC TTTGACGGCG ACAGTGACAG CGACAGCCAA
780

AGCAGGGTCC GAAACCAAGG CGGGCTGCCA GGGGCTGTTC ACCAGAACGG GCGTTGCCGG
840

35 CCTGAGACTG GCGCGGTTGG CAAAGACAGC GATGGCTGCT ACGTGCAACT TCCACGTTCC
900

CGGCCTGCCC TGGAGCTGAC GCGCTGACG GCTCCTGGGC CGGGATCCGG CTCCCGGCCC

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960

ACCCAGGCCA AGCTGCTGGC TAAGAAGCGC GTGAAACGAA TGTGCTGGT GATCGTTGTG
1020

5 CTTTTTTTC TGTGTTGGTT GCCAGTTTAT AGTGCCAACA CGTGGCGCGC CTTTGATGGC
1080

CCGGGTGCAC ACCGAGCACT CTCGGGTGCT CCTATCTCCT TCATTCACTT GCTGAGCTAC
1140

GCCTCGGCCT GTGTCAACCC CCTGGTCTAC TGCTTCATGC ACCGTCGCTT TCGCCAGGCC
1200

10 TGCCTGGAAA CTTGCGCTCG CTGCTGCCCC CGGCCTCCAC GAGCTCGCCC CAGGGCTCTT
1260

CCCGATGAGG ACCCTCCAC TCCCTCCATT GCTTCGCTGT CCAGGCTTAG CTACACCACC
1320

15 ATCAGCACAC TGGGCCCTGG CTGA
1344

(133) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 447 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

25 Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1 5 10 15
Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
20 25 30
Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
35 40 45
30 Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
50 55 60
Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
65 70 75 80
35 Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
85 90 95
Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu

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	100	105	110
	Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys 115 120 125		
5	Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser 130 135 140		
	Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu 145 150 155 160		
	Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val 165 170 175		
10	Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr 180 185 190		
	Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg 195 200 205		
15	Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu 210 215 220		
	Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu 225 230 235 240		
	Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp 245 250 255		
20	Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala 260 265 270		
	Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys 275 280 285		
25	Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu 290 295 300		
	Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro 305 310 315 320		
	Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu 325 330 335		
30	Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala 340 345 350		
	Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser 355 360 365		
35	Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys 370 375 380		
	Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala 385 390 395 400		

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Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
 405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser
 420 425 430

5 Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
 435 440 445

(134) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

15 ATGAACAGCA CATGTATTGA AGAACAGCAT GACCTGGATC ACTATTGTGTT TCCCATTGTT 60
 TACATCTTTG TGATTATAGT CAGCATTCCA GCCAATATTG GATCTCTGTG TGTGTCTTTC 120
 CTGCAAGCAA AGAAGGAAAG TGAAC TAGGA ATTTACCTCT TCAGTTTGTC ACTATCAGAT 180
 TTACTCTATG CATTAACTCT CCCTTTATGG ATTGATTATA CTTGGAATAA AGACAACTGG 240
 ACTTTCTCTC CTGCCTTGTG CAAAGGGAGT GCTTTTCTCA TGTACATGAA TTTTACAGC 300
 20 AGCACAGCAT TCCTCACCTG CATTGCCGTT GATCGGTATT TGGCTGTTGT CTACCCCTTG 360
 AAGTTTTTTT TCCTAAGGAC AAGAAGATTT GCACTCATGG TCAGCCTGTC CATCTGGATA 420
 TTGGAACCA TCTTCAATGC TGTTCATGTTG TGGGAAGATG AACAGTTGT TGAATATTGC 480
 GATGCCGAAA AGTCTAATTT TACTTTATGC TATGACAAAT ACCCTTTAGA GAAATGGCAA 540
 ATCAACCTCA ACTTGTTTCAG GACGTGTACA GGCTATGCAA TACCTTTGGT CACCATCCTG 600
 25 ATCTGTAACC GGAAAGTCTA CCAAGCTGTG CGGCACAATA AAGCCACGGA AAACAAGGAA 660
 AAGAAGAGAA TCAAAAACT ACTTGTCAGC ATCACAGTTA CTTTGTCTT ATGCTTTACT 720
 CCCTTTCATG TGATGTTGCT GATTCGCTGC ATTTTAGAGC ATGCTGTGAA CTTGAAGAC 780
 CACAGCAATT CTGGGAAGCG AACTTACACA ATGTATAGAA TCACGGTTGC ATTAACAAGT 840
 TTAAATTGTG TTGCTGATCC AATTCTGTAC TGTTTTGTTA CCGAAACAGG AAGATATGAT 900
 30 ATGTGGAATA TATTAAATTT CTGCACTGGG AGGTGTAATA CATCACAAAG ACAAGAAAA 960
 CGCATACTTT CTGTGTCTAC AAAAGATACT ATGGAATTAG AGGTCCTTGA GTAG 1014

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(135) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

10 Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu
 1 5 10 15
 Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn
 20 25 30
 Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Ala Lys Lys Glu Ser Glu
 35 40 45
 15 Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
 50 55 60
 Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
 65 70 75 80
 20 Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met
 85 90 95
 Asn Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg
 100 105 110
 Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg
 115 120 125
 25 Arg Phe Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile
 130 135 140
 Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys
 145 150 155 160
 30 Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu
 165 170 175
 Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr
 180 185 190
 Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln
 195 200 205
 35 Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile
 210 215 220

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Lys Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr
 225 230 235 240
 Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val
 245 250 255
 5 Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr
 260 265 270
 Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
 275 280 285
 10 Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile
 290 295 300
 Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys
 305 310 315 320
 Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu
 325 330 335
 15 Glu

(136) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 999 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

25 ATGGTGAAC CCACCCACCG TGGGATGCAC ACTTCTCTGC ACCTCTGGAA CCGCAGCAGT
 60
 TACAGACTGC ACAGCAATGC CAGTGAGTCC CTTGGAAAAG GCTACTCTGA TGGAGGGTGC
 120
 TACGAGCAAC TTTTGTCTC TCCTGAGGTG TTTGTGACTC TGGGTGTCAT CAGCTTGTTG
 30 180
 GAGAATATCT TAGTGATTGT GGCAATAGCC AAGAACAAGA ATCTGCATT CACCATGTAC
 240
 TTTTTCATCT GCAGCTTGGC TGTGGCTGAT ATGCTGGTGA GCGTTTCAAA TGGATCAGAA
 300
 35 ACCATTATCA TCACCCTATT AAACAGTACA GATACGGATG CACAGAGTTT CACAGTGAAT
 360

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ATTGATAATG TCATTGACTC GGTGATCTGT AGCTCCTTGC TTGCATCCAT TTGCAGCCTG
420

CTTTCAATTG CAGTGGACAG GTACTTTACT ATCTTCTATG CTCTCCAGTA CCATAACATT
480

5 ATGACAGTTA AGCGGGTTGG GATCAGCATA AGTTGTATCT GGGCAGCTTG CACGGTTTCA
540

GGCATTTTGT TCATCATTTA CTCAGATAGT AGTGCTGTCA TCATCTGCCT CATCACCATG
600

10 TTCTTCACCA TGCTGGCTCT CATGGCTTCT CTCTATGTCC ACATGTTCTT GATGGCCAGG
660

CTTCACATTA AGAGGATTGC TGTCTCCCC GGCACCTGGT CCATCCGCCA AGGTGCCAAT
720

ATGAAGGGAA AAATTACCTT GACCATCCTG ATTGGCGTCT TTGTTGTCTG CTGGGCCCCA
780

15 TTCTTCCTCC ACTTAATATT CTACATCTCT TGTCTCAGA ATCCATATTG TGTGTGCTTC
840

ATGTCTCACT TTAACCTGTA TCTCATACTG ATCATGTGTA ATTCAATCAT CGATCCTCTG
900

ATTTATGCAC TCCGGAGTCA AGAACTGAGG AAAACCTTCA AAGAGATCAT CTGTTGCTAT
20 960

CCCCTGGGAG GCCTTTGTGA CTTGTCTAGC AGATATTAA
999

(137) INFORMATION FOR SEQ ID NO:136:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Val	Asn	Ser	Thr	His	Arg	Gly	Met	His	Thr	Ser	Leu	His	Leu	Trp
1				5				10					15		
Asn	Arg	Ser	Ser	Tyr	Arg	Leu	His	Ser	Asn	Ala	Ser	Glu	Ser	Leu	Gly
		20					25					30			
Lys	Gly	Tyr	Ser	Asp	Gly	Gly	Cys	Tyr	Glu	Gln	Leu	Phe	Val	Ser	Pro
	35					40					45				

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	Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu	
	50	55 60
	Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr	
	65	70 75 80
5	Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser	
		85 90 95
	Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr	
		100 105 110
10	Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val	
		115 120 125
	Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala	
		130 135 140
	Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile	
		145 150 155 160
15	Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala	
		165 170 175
	Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala	
		180 185 190
20	Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met	
		195 200 205
	Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys	
		210 215 220
	Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn	
		225 230 235 240
25	Met Lys Gly Lys Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val	
		245 250 255
	Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro	
		260 265 270
30	Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu	
		275 280 285
	Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu	
		290 295 300
	Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr	
		305 310 315 320
35	Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr	
		325 330

(138) INFORMATION FOR SEQ ID NO:137:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCCAATATGA AGGGAAAAAT TACCTTGACC ATC
33

10 (137) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T
31

20 (140) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ATGGGGCCCA CCCTAGCGGT TCCCACCCCC TATGGCTGTA TTGGCTGTAA GCTACCCCAG 60
CCAGAATACC CACCGGCTCT AATCATCTTT ATGTTCTGCG CGATGGTTAT CACCATCGTT 120
30 GTAGACCTAA TCGGCAACTC CATGGTCATT TTGGCTGTGA CGAAGAACAA GAAGCTCCGG 180
AATTCTGGCA ACATCTTCGT GGTCAGTCTC TCTGTGGCCG ATATGCTGGT GGCCATCTAC 240
CCATACCCTT TGATGCTGCA TGCCATGTCC ATTGGGGGCT GGGATCTGAG CCAGTTACAG 300
TGCCAGATGG TCGGGTTCAT CACAGGGCTG AGTGTGGTCG GCTCCATCTT CAACATCGTG 360

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	GCAATCGCTA TCAACCGTTA CTGCTACATC TGCCACAGCC TCCAGTACGA ACGGATCTTC	420
	AGTGTGCGCA ATACCTGCAT CTACCTGGTC ATCACCTGGA TCATGACCGT CCTGGCTGTC	480
	CTGCCCAACA TGTACATTGG CACCATCGAG TACGATCCTC GCACCTACAC CTGCATCTTC	540
	AACTATCTGA ACAACCCTGT CTTCACTGTT ACCATCGTCT GCATCCACTT CGTCCTCCCT	600
5	CTCCTCATCG TGGGTTTCTG CTACGTGAGG ATCTGGACCA AAGTGCTGGC GGCCCGTGAC	660
	CCTGCAGGGC AGAATCCTGA CAACCAACTT GCTGAGGTTC GCAATTTTCT AACCATGTTT	720
	GTGATCTTCC TCCTCTTTGC AGTGTGCTGG TGCCCTATCA ACGTGCTCAC TGTCTTGGTG	780
	GCTGTCACTC CGAAGGAGAT GGCAGGCAAG ATCCCCAACT GGCTTTATCT TGCAGCCTAC	840
	TTCATAGCCT ACTTCAACAG CTGCCTCAAC GCTGTGATCT ACGGGCTCCT CAATGAGAAT	900
10	TTCCGAAGAG AATACTGGAC CATCTTCCAT GCTATGCGGC ACCCTATCAT ATTCTTCCCT	960
	GGCCTCATCA GTGATATTCG TGAGATGCAG GAGGCCCGTA CCCTGGCCCG CGCCCGTGCC	1020
	CATGCTCGCG ACCAAGCTCG TGAACAAGAC CGTGCCCATG CCTGTCCTGC TGTGGAGGAA	1080
	ACCCCGATGA ATGTCCGGAA TGTTCATTA CCTGGTGATG CTGCAGCTGG CCACCCCGAC	1140
	CGTGCTCTG GCCACCCTAA GCCCCATTCC AGATCCTCCT CTGCCTATCG CAAATCTGCC	1200
15	TCTACCCACC ACAAGTCTGT CTTAGCCAC TCCAAGGCTG CCTCTGGTCA CCTCAAGCCT	1260
	GTCTCTGGCC ACTCCAAGCC TGCCTCTGGT CACCCCAAGT CTGCCACTGT CTACCCTAAG	1320
	CCTGCCTCTG TCCATTTCAA GGGTGACTCT GTCCATTTCA AGGGTGACTC TGTCCATTTC	1380
	AAGCCTGACT CTGTTCAATT CAAGCCTGCT TCCAGCAACC CCAAGCCCAT CACTGGCCAC	1440
	CATGTCTCTG CTGGCAGCCA CTCCAAGTCT GCCTTCAGTG CTGCCACCAG CCACCCTAAA	1500
20	CCCATCAAGC CAGCTACCAG CCATGCTGAG CCCACCACTG CTGACTATCC CAAGCCTGCC	1560
	ACTACCAGCC ACCCTAAGCC CGCTGCTGCT GACAACCCTG AGCTCTCTGC CTCCCATTGC	1620
	CCCGAGATCC CTGCCATTGC CCACCCTGTG TCTGACGACA GTGACCTCCC TGAGTCGGCC	1680
	TCTAGCCCTG CCGCTGGGCC CACCAAGCCT GCTGCCAGCC AGCTGGAGTC TGACACCATC	1740
	GCTGACCTTC CTGACCCTAC TGTAGTCACT ACCAGTACCA ATGATTACCA TGATGTCGTG	1800
25	GTTGTTGATG TTGAAGATGA TCCTGATGAA ATGGCTGTGT GA	1842

(141) INFORMATION FOR SEQ ID NO:140:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

5	Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys	1	5	10	15
	Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe	20	25	30	
10	Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met	35	40	45	
	Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn	50	55	60	
	Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr	65	70	75	80
15	Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu	85	90	95	
	Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val	100	105	110	
20	Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys	115	120	125	
	Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn	130	135	140	
	Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val	145	150	155	160
25	Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr	165	170	175	
	Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile	180	185	190	
30	Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr	195	200	205	
	Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln	210	215	220	
	Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe	225	230	235	240
35	Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu	245	250	255	

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	Thr	Val	Leu	Val	Ala	Val	Ser	Pro	Lys	Glu	Met	Ala	Gly	Lys	Ile	Pro	
				260					265					270			
	Asn	Trp	Leu	Tyr	Leu	Ala	Ala	Tyr	Phe	Ile	Ala	Tyr	Phe	Asn	Ser	Cys	
			275					280					285				
5	Leu	Asn	Ala	Val	Ile	Tyr	Gly	Leu	Leu	Asn	Glu	Asn	Phe	Arg	Arg	Glu	
		290					295					300					
	Tyr	Trp	Thr	Ile	Phe	His	Ala	Met	Arg	His	Pro	Ile	Ile	Phe	Phe	Pro	
	305					310					315					320	
	Gly	Leu	Ile	Ser	Asp	Ile	Arg	Glu	Met	Gln	Glu	Ala	Arg	Thr	Leu	Ala	
10					325					330					335		
	Arg	Ala	Arg	Ala	His	Ala	Arg	Asp	Gln	Ala	Arg	Glu	Gln	Asp	Arg	Ala	
				340					345					350			
	His	Ala	Cys	Pro	Ala	Val	Glu	Glu	Thr	Pro	Met	Asn	Val	Arg	Asn	Val	
			355					360					365				
15	Pro	Leu	Pro	Gly	Asp	Ala	Ala	Ala	Gly	His	Pro	Asp	Arg	Ala	Ser	Gly	
		370				375						380					
	His	Pro	Lys	Pro	His	Ser	Arg	Ser	Ser	Ser	Ala	Tyr	Arg	Lys	Ser	Ala	
	385					390					395					400	
	Ser	Thr	His	His	Lys	Ser	Val	Phe	Ser	His	Ser	Lys	Ala	Ala	Ser	Gly	
20					405					410					415		
	His	Leu	Lys	Pro	Val	Ser	Gly	His	Ser	Lys	Pro	Ala	Ser	Gly	His	Pro	
				420					425					430			
	Lys	Ser	Ala	Thr	Val	Tyr	Pro	Lys	Pro	Ala	Ser	Val	His	Phe	Lys	Gly	
			435					440					445				
25	Asp	Ser	Val	His	Phe	Lys	Gly	Asp	Ser	Val	His	Phe	Lys	Pro	Asp	Ser	
		450					455					460					
	Val	His	Phe	Lys	Pro	Ala	Ser	Ser	Asn	Pro	Lys	Pro	Ile	Thr	Gly	His	
	465					470					475					480	
	His	Val	Ser	Ala	Gly	Ser	His	Ser	Lys	Ser	Ala	Phe	Ser	Ala	Ala	Thr	
30					485					490					495		
	Ser	His	Pro	Lys	Pro	Ile	Lys	Pro	Ala	Thr	Ser	His	Ala	Glu	Pro	Thr	
				500					505					510			
	Thr	Ala	Asp	Tyr	Pro	Lys	Pro	Ala	Thr	Thr	Ser	His	Pro	Lys	Pro	Ala	
		515						520					525				
35	Ala	Ala	Asp	Asn	Pro	Glu	Leu	Ser	Ala	Ser	His	Cys	Pro	Glu	Ile	Pro	
		530					535					540					
	Ala	Ile	Ala	His	Pro	Val	Ser	Asp	Asp	Ser	Asp	Leu	Pro	Glu	Ser	Ala	

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545 550 555 560
 Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu
 565 570 575
 Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser
 5 580 585 590
 Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro
 595 600 605
 Asp Glu Met Ala Val
 610

10 (142) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ATGGGGCCCCA CCCTAGCGGT TCCCACCCCC TATGGCTGTA TTGGCTGTAA GCTACCCCAG 60
 CCAGAATACC CACCGGCTCT AATCATCTTT ATGTTCTGCG CGATGGTTAT CACCATCGTT 120
 20 GTAGACCTAA TCGGCAACTC CATGGTCATT TTGGCTGTGA CGAAGAACAA GAAGCTCCGG 180
 AATTCTGGCA ACATCTTCGT GGTCAGTCTC TCTGTGGCCG ATATGCTGGT GGCCATCTAC 240
 CCATACCCTT TGATGCTGCA TGCCATGTCC ATTGGGGGCT GGGATCTGAG CCAGTTACAG 300
 TGCCAGATGG TCGGGTTCAT CACAGGGCTG AGTGTGGTCG GCTCCATCTT CAACATCGTG 360
 GCAATCGCTA TCAACCGTTA CTGCTACATC TGCCACAGCC TCCAGTACGA ACGGATCTTC 420
 25 AGTGTGCGCA ATACCTGCAT CTACCTGGTC ATCACCTGGA TCATGACCGT CCTGGCTGTC 480
 CTGCCCCAACA TGTACATTGG CACCATCGAG TACGATCCTC GCACCTACAC CTGCATCTTC 540
 AACTATCTGA ACAACCCTGT CTTCACTGTT ACCATCGTCT GCATCCACTT CGTCCTCCCT 600
 CTCCTCATCG TGGGTTTCTG CTACGTGAGG ATCTGGACCA AAGTGCTGGC GGCCCGTGAC 660
 CCTGCAGGGC AGAATCCTGA CAACCAACTT GCTGAGGTTC GCAATAAACT AACCATGTTT 720
 30 GTGATCTTCC TCCTCTTTGC AGTGTGCTGG TGCCCTATCA ACGTGCTCAC TGTCTGGTG 780
 GCTGTCAGTC CGAAGGAGAT GGCAGGCAAG ATCCCCAACT GGCTTTATCT TGCAGCCTAC 840

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TTCATAGCCT ACTTCAACAG CTGCCTCAAC GCTGTGATCT ACGGGCTCCT CAATGAGAAT 900
 TTCCGAAGAG AATACTGGAC CATCTTCCAT GCTATGCGGC ACCCTATCAT ATTCTTCTCT 960
 GGCCTCATCA GTGATATTCG TGAGATGCAG GAGGCCCCGTA CCCTGGCCCCG CGCCCCGTGCC 1020
 CATGCTCGCG ACCAAGCTCG TGAACAAGAC CGTGCCCATG CCTGTCTCTGC TGTGGAGGAA 1080
 5 ACCCCGATGA ATGTCCGGAA TGTTCATTATTA CCTGGTGATG CTGCAGCTGG CCACCCCGAC 1140
 CGTGCTCTG GCCACCCTAA GCCCCATTCC AGATCCTCCT CTGCCTATCG CAAATCTGCC 1200
 TCTACCCACC ACAAGTCTGT CTTTAGCCAC TCCAAGGCTG CCTCTGGTCA CCTCAAGCCT 1260
 GTCTCTGGCC ACTCCAAGCC TGCCTCTGGT CACCCCAAGT CTGCCACTGT CTACCCTAAG 1320
 CCTGCCTCTG TCCATTTCAA GGCTGACTCT GTCCATTTCA AGGGTGACTC TGTCCATTTT 1380
 10 AAGCCTGACT CTGTTTCATT CAAGCCTGCT TCCAGCAACC CCAAGCCCAT CACTGGCCAC 1440
 CATGTCTCTG CTGGCAGCCA CTCCAAGTCT GCCTTCAATG CTGCCACCAG CCACCCTAAA 1500
 CCCATCAAGC CAGCTACCAG CCATGCTGAG CCCACCACTG CTGACTATCC CAAGCCTGCC 1560
 ACTACCAGCC ACCCTAAGCC CGCTGCTGCT GACAACCCTG AGCTCTCTGC CTCCCATTGC 1620
 CCGGAGATCC CTGCCATTGC CCACCCTGTG TCTGACGACA GTGACCTCCC TGAGTCGGCC 1680
 15 TCTAGCCCTG CCGCTGGGCC CACCAAGCCT GCTGCCAGCC AGCTGGAGTC TGACACCATC 1740
 GCTGACCTTC CTGACCCTAC TGTAGTCACT ACCAGTACCA ATGATTACCA TGATGTCGTG 1800
 GTTGTGATG TTGAAGATGA TCCTGATGAA ATGGCTGTGT GA 1842

(143) INFORMATION FOR SEQ ID NO:142:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 613 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
 1 5 10 15

Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
 20 25 30

30 Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
 35 40 45

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	Val	Ile	Leu	Ala	Val	Thr	Lys	Asn	Lys	Lys	Leu	Arg	Asn	Ser	Gly	Asn	
	50						55					60					
	Ile	Phe	Val	Val	Ser	Leu	Ser	Val	Ala	Asp	Met	Leu	Val	Ala	Ile	Tyr	
	65					70					75					80	
5	Pro	Tyr	Pro	Leu	Met	Leu	His	Ala	Met	Ser	Ile	Gly	Gly	Trp	Asp	Leu	
					85					90					95		
	Ser	Gln	Leu	Gln	Cys	Gln	Met	Val	Gly	Phe	Ile	Thr	Gly	Leu	Ser	Val	
				100					105					110			
10	Val	Gly	Ser	Ile	Phe	Asn	Ile	Val	Ala	Ile	Ala	Ile	Asn	Arg	Tyr	Cys	
			115					120					125				
	Tyr	Ile	Cys	His	Ser	Leu	Gln	Tyr	Glu	Arg	Ile	Phe	Ser	Val	Arg	Asn	
	130						135					140					
	Thr	Cys	Ile	Tyr	Leu	Val	Ile	Thr	Trp	Ile	Met	Thr	Val	Leu	Ala	Val	
	145					150					155					160	
15	Leu	Pro	Asn	Met	Tyr	Ile	Gly	Thr	Ile	Glu	Tyr	Asp	Pro	Arg	Thr	Tyr	
					165					170					175		
	Thr	Cys	Ile	Phe	Asn	Tyr	Leu	Asn	Asn	Pro	Val	Phe	Thr	Val	Thr	Ile	
				180					185					190			
20	Val	Cys	Ile	His	Phe	Val	Leu	Pro	Leu	Leu	Ile	Val	Gly	Phe	Cys	Tyr	
			195					200					205				
	Val	Arg	Ile	Trp	Thr	Lys	Val	Leu	Ala	Ala	Arg	Asp	Pro	Ala	Gly	Gln	
	210						215					220					
	Asn	Pro	Asp	Asn	Gln	Leu	Ala	Glu	Val	Arg	Asn	Lys	Leu	Thr	Met	Phe	
	225				230						235					240	
25	Val	Ile	Phe	Leu	Leu	Phe	Ala	Val	Cys	Trp	Cys	Pro	Ile	Asn	Val	Leu	
					245					250					255		
	Thr	Val	Leu	Val	Ala	Val	Ser	Pro	Lys	Glu	Met	Ala	Gly	Lys	Ile	Pro	
				260					265					270			
30	Asn	Trp	Leu	Tyr	Leu	Ala	Ala	Tyr	Phe	Ile	Ala	Tyr	Phe	Asn	Ser	Cys	
		275						280					285				
	Leu	Asn	Ala	Val	Ile	Tyr	Gly	Leu	Leu	Asn	Glu	Asn	Phe	Arg	Arg	Glu	
	290						295					300					
	Tyr	Trp	Thr	Ile	Phe	His	Ala	Met	Arg	His	Pro	Ile	Ile	Phe	Phe	Ser	
	305					310					315					320	
35	Gly	Leu	Ile	Ser	Asp	Ile	Arg	Glu	Met	Gln	Glu	Ala	Arg	Thr	Leu	Ala	
					325					330					335		
	Arg	Ala	Arg	Ala	His	Ala	Arg	Asp	Gln	Ala	Arg	Glu	Gln	Asp	Arg	Ala	

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	340	345	350
	His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val		
	355	360	365
5	Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly		
	370	375	380
	His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala		
	385	390	395
	Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly		
	405	410	415
10	His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro		
	420	425	430
	Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Ala		
	435	440	445
15	Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser		
	450	455	460
	Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His		
	465	470	475
	His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Asn Ala Ala Thr		
	485	490	495
20	Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr		
	500	505	510
	Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala		
	515	520	525
25	Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro		
	530	535	540
	Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala		
	545	550	555
	Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu		
	565	570	575
30	Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser		
	580	585	590
	Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro		
	595	600	605
35	Asp Glu Met Ala Val		
	610		

(144) INFORMATION FOR SEQ ID NO:143:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GCTGAGGTTC GCAATAAACT AACCATGTTT GTG

33

(145) INFORMATION FOR SEQ ID NO:144:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T

31

(146) INFORMATION FOR SEQ ID NO:145:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 25 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTAGATATCG GGGCCACCC TAGCGGT

33

(147) INFORMATION FOR SEQ ID NO:146:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

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(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGTACCCCCA CAGCCATTTC ATCAGGATC

33